

;; CURRENT FILING DATE: 1998-10-21
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PERL Program
;; SEQ ID NO 5
;; LENGTH: 1506
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE: -
;; OTHER INFORMATION: 1250374
US-09-176-657-5

Query Match 2.2%; Score 29; DB 3; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 484 ACCGTGTAGAGAGCCGTAATCGAGGT 512
DB 717 ACCGTGTAGAGAGCCGTAATCGAGGT 745

RESULT 3

US-09-421-299-5
; Sequence 5, Application US/09421299
; Patent No. 6524579
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aime
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/421,299
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: 09/176,657
; EARLIER FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-421-299-5

Query Match

Best Local Similarity 2.2%; Score 29; DB 4; Length 1506;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 484 ACCGTGTAGAGAGCCGTAATCGAGGT 512
DB 717 ACCGTGTAGAGAGCCGTAATCGAGGT 745

RESULT 4

US-09-620-312D-462/C
; Sequence 462, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Peiyan
; APPLICANT: Chen, Ruihong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping

;; APPLICANT: Ma, Yungqing
;; APPLICANT: Wang, Dunrui
;; APPLICANT: Wang, Zhiwei
;; APPLICANT: John Tillinghast
;; APPLICANT: Drmanac, Radoje T.
;; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
;; FILE REFERENCE: 784CIP2B Polypeptides
;; CURRENT APPLICATION NUMBER: US/09/620,312D
;; CURRENT FILING DATE: 2000-07-19
;; PRIOR APPLICATION NUMBER: 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; NUMBER OF SEQ ID NOS: 1105
;; SOFTWARE: perl_genes Version 1.0
;; SEQ ID NO 462
;; LENGTH: 1946
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1404)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1946)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-462

Query Match 2.1%; Score 28; DB 4; Length 1946;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1172 CAAAAACAAACAAACAAACAAAC 1199
DB 1609 CAAAAACAAACAAACAAACAAAC 1582

RESULT 5

US-09-685-853A-3/C
; Sequence 3, Application US/09685853A
; Patent No. 6479270
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; FILE REFERENCE: CLO00871 AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/685,853A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/182,194
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 74962
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(74962)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-853A-3

Query Match 2.0%; Score 27; DB 4; Length 74962;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1289 CAACGAAAAAAAAAAAAAAAAAAAA 1315
DB 28548 CAACGAAAAAAAAAAAAAAAAAAAA 28522

RESULT 6
US-09-306-290-6/c
; Sequence 6, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer RGP
US-09-306-290-6

Query Match 1.9%; Score 26; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1288 ACAACGAAAAAAAAAAAAAAAAAAAA 1313
Db 26 ACAACGAAAAAAAAAAAAAAAAAAAA 1

RESULT 7
US-09-105-542A-12
; Sequence 12, Application US/09105542A
; Patent No. 6323329
; GENERAL INFORMATION:
; APPLICANT: Bullerdiek, Jörn
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES OF GENES OF THE
; FILE REFERENCE: BOEHA.001C1CP
; CURRENT APPLICATION NUMBER: US/09/105,542A
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/DE96/02494
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(528)
; OTHER INFORMATION: n = A,T,C or G
US-09-105-542A-12

Query Match 1.9%; Score 26; DB 4; Length 528;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 472 AACGAAAAAAAAAAAAAAAAAAAA 497

RESULT 8
US-08-341-568-1
; Sequence 1, Application US/08341568
; Patent No. 5661021
; GENERAL INFORMATION:
; APPLICANT: Buchert, Johanna
; APPLICANT: Silka-aho, Matti

APPLICANT: Viikari, Liisa
APPLICANT: Penttilä, Merja
APPLICANT: Saloheimo, Anu
APPLICANT: Marjatta, Ranna
TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching
TITLE OF INVENTION: pulps
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
STATE: VA
COUNTRY: US
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: OM9414
US-08-341-568-1

Query Match 1.9%; Score 26; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 460 AACGAAAAAAAAAAAAAAAAAAAA 485

RESULT 9
US-08-911-020-1
; Sequence 1, Application US/08911020
; Patent No. 5854047
; GENERAL INFORMATION:
; APPLICANT: Buchert, Johanna
; APPLICANT: Silka-aho, Matti
; APPLICANT: Viikari, Liisa
; APPLICANT: Penttilä, Merja
; APPLICANT: Saloheimo, Anu
; APPLICANT: Marjatta, Ranna
TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching
TITLE OF INVENTION: lignocellulosic pulps
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
STATE: VA

COUNTRY: US
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911.020
FILING DATE: 13-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/341,568
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Trichoderma reesei
STRAIN: QM9414
US-08-911-020-1

Query Match 1.9%; Score 26; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
|||||
DB 460 AACGAAAAAAAAAAAAAAAAAAAA 485

RESULT 10
US-09-328-111-361/c
Sequence 361, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Dertl, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328.111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 361
LENGTH: 631
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)---(631)
OTHER INFORMATION: n - A,T,C or G
US-09-328-111-361

Query Match 1.9%; Score 26; DB 3; Length 631;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
|||||
DB 44 AACGAAAAAAAAAAAAAAAAAAAA 19

RESULT 11
US-08-630-118A-1
Sequence 1, Application US/08630118A
Patent No. 591901
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yange
APPLICANT: McCaleb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630.118A
FILING DATE: April 8, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 248..1582
US-08-630-118A-1

Query Match 1.9%; Score 26; DB 2; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
|||||
DB 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 12
US-08-838-399-1
; Sequence 1, Application US/08838399
; Patent No. 5965392
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCalieb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 248..1585
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 248..1582
; US-08-838-399-1

Query Match 1.9%; Score 26; DB 2; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 13
US-09-235-839-1
; Sequence 1, Application US/09235839
; Patent No. 6207799
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCalieb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.

; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,839
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,118
; FILING DATE: April 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 96,149-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 248..1582
; US-09-235-839-1

Query Match 1.9%; Score 26; DB 3; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 14
US-09-327-035-1
; Sequence 1, Application US/09327035
; Patent No. 6368824
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCalieb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/327.035
FILING DATE: 07-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,399
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 248..1585
NAME/KEY: mat_peptide
LOCATION: 248..1582
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-327-035-1

Query Match 1.9%; Score 26; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 15
US-08-630-118A-3
Sequence 3, Application US/08630118A
Patent No. 5919901
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yingshe
APPLICANT: McCaleb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,118A
FILING DATE: April 8, 1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 371..1705
US-08-630-118A-3

Query Match 1.9%; Score 26; DB 2; Length 2604;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2538 AACGAAAAAAAAAAAAAAAAAAAA 2563

Search completed: September 25, 2003, 11:41:02
Job time : 88 secs

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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:02:54 ; Search time 329 Seconds
(without alignments)
10139.568 Million cell updates/sec

Title: US-09-809-545a-1
Perfect score: 1340
Sequence: 1 ggcgcgcgcgcgcgcacacat.....ggccgaagggttcgctag 1340

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

ord size : 0

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1340	100.0	1340	US-09-809-545a-1	Sequence 1, Appl
2	70	5.2	2372	9 US-09-794-591-1	Sequence 1, Appl
3	48	3.6	120	US-09-908-975-7420	Sequence 7420, Ap
4	32	2.4	125	9 US-09-864-761-28375	Sequence 28375, A
5	32	2.4	1574	9 US-09-864-761-11604	Sequence 11804, A
6	30	2.2	1574	9 US-09-925-302-42	Sequence 42, Appl
7	30	2.2	5898	12 US-10-311-455-1913	Sequence 1913, Ap
8	30	2.2	5898	12 US-10-240-453-203	Sequence 203, Ap
9	30	2.2	5898	14 US-10-239-676-179	Sequence 179, App
10	30	2.2	6126	12 US-10-311-455-1878	Sequence 1804, Ap
11	30	2.2	6126	12 US-10-311-455-12704	Sequence 1278, Ap
12	30	2.2	6510	12 US-10-311-455-367	Sequence 367, App
13	30	2.2	2940917	13 US-10-027-632-174763	Sequence 174763, A
14	29	2.2	1506	12 US-10-359-385-5	Sequence 5, Appl
15	29	2.2	4274	12 US-10-311-455-2039	Sequence 2039, Ap
16	29	2.2	6211	12 US-10-311-455-779	Sequence 779, App

C 17	29	2.2	14112	12	US-10-311-455-1416	Sequence 1416, Ap
C 18	28	2.1	289	10	US-09-960-352-289	Sequence 289, App
C 19	28	2.1	1946	14	US-10-037-270-462	Sequence 462, App
C 20	27	2.0	177	10	US-09-867-701-9672	Sequence 9672, Ap
C 21	27	2.0	214	10	US-09-883-965-591	Sequence 591, App
C 22	27	2.0	263	10	US-09-867-701-9696	Sequence 9696, Ap
C 23	27	2.0	308	10	US-09-960-352-714	Sequence 714, App
C 24	27	2.0	315	10	US-09-960-352-12366	Sequence 12366, A
C 25	27	2.0	337	10	US-09-960-352-7832	Sequence 7832, Ap
C 26	27	2.0	344	10	US-09-960-352-7833	Sequence 7833, Ap
C 27	27	2.0	349	10	US-09-960-352-11398	Sequence 11398, A
C 28	27	2.0	382	10	US-09-960-352-10167	Sequence 10167, A
C 29	27	2.0	383	10	US-09-960-352-13506	Sequence 13506, A
C 30	27	2.0	388	10	US-09-960-352-6680	Sequence 6680, Ap
C 31	27	2.0	394	9	US-09-817-318-16	Sequence 16, Appl
C 32	27	2.0	411	10	US-09-960-352-3551	Sequence 3551, Ap
C 33	27	2.0	414	11	US-09-918-995-17603	Sequence 17603, A
C 34	27	2.0	418	10	US-09-960-352-10650	Sequence 10650, A
C 35	27	2.0	419	10	US-09-960-352-13041	Sequence 13041, A
C 36	27	2.0	434	10	US-09-960-352-12123	Sequence 12123, A
C 37	27	2.0	438	10	US-09-924-035A-516	Sequence 516, App
C 38	27	2.0	533	12	US-09-814-353-16498	Sequence 16498, A
C 39	27	2.0	1619	12	US-09-873-367C-329	Sequence 329, App
C 40	27	2.0	5532	12	US-10-311-455-751	Sequence 751, App
C 41	27	2.0	6046	12	US-10-240-453-24	Sequence 24, Appl
C 42	27	2.0	6046	14	US-10-239-676-16	Sequence 16, Appl
C 43	27	2.0	6069	12	US-10-240-453-194	Sequence 194, App
C 44	27	2.0	6069	14	US-10-239-676-172	Sequence 172, App
C 45	27	2.0	6135	12	US-10-311-455-1346	Sequence 1346, Ap

ALIGNMENTS

RESULT 1
US-09-809-545a-1
; Sequence 1, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ. ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 1
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-809-545a-1

Query Match 100.0%; Score 1340; DB 10; Length 1340;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCGCGCGCCCTTACACAAATGGCTCATCTATCCCTCAGGCGATTGCTCCACCCAGA	60
DB	1	GGCGCGCGCCCTTACACAAATGGCTCATCTATCCCTCAGGCGATTGCTCCACCCAGA	60
QY	61	ATGCGATCGTCGAGATATACAGGCGCCCTTCCCATCCGCGCAGAGACCGGCAG	120
DB	61	ATGCGATCGTCGAGATATACAGGCGCCCTTCCCATCCGCGCAGAGACCGGCAG	120
QY	121	CCGACTGTCGCCGACACATTAACCTGATCTCTCTACAGACGCACTGGAGAGAG	180
DB	121	CCGACTGTCGCCGACACATTAACCTGATCTCTCTACAGACGCACTGGAGAGAG	180
QY	181	CGGTTATACAGGCGACGCGCTCTCCGACCGCACACAGACAGATGATGCGGCCCG	240
DB	181	CGGTTATACAGGCGACGCGCTCTCCGACCGCACACAGACAGATGATGCGGCCCG	240

Oy 1045 GATCCAGACTAGGAGCCATGATGATGCTCTGTTCTTCT 1092
|||||
Db 13 GATCCAGACTAGGAGCCATGATGATGCTCTGTTCTTCT 60

RESULT 4
US-09-864-761-28375
; Sequence 28375, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28375
; LENGTH: 125
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006075.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
; OTHER INFORMATION: EST HUMAN HIT: 225303.1, EVALUATE 9.00e-61
; OTHER INFORMATION: NT HIT: g11431054, EVALUATE 2.00e-64
; OTHER INFORMATION: SWISSPROT HIT: P54537, EVALUATE 1.40e+00
US-09-864-761-28375

Query Match 2.4%; Score 32; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 247 GGCCAGCCCCAGACACACTTCTGAAAAACAC 278
|||||
Db 9 GGCCAGCCCCAGACACACTTCTGAAAAACAC 40
RESULT 5
US-09-864-761-11804
; Sequence 11804, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11804
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006075.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
US-09-864-761-11804

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Query Match      2.4%; Score 32; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      247 GGGCAGCCCGACACACCTTCTGAAACAC 278
DB      296 GGGCAGCCCGACACACCTTCTGAAACAC 327

RESULT 6
US-09-925-302-42
; Sequence 42, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42
; LENGTH: 1574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1029)
; NAME/KEY: n equals a,t,g, or c
; LOCATION: (1076)
; NAME/KEY: misc feature
; LOCATION: (1574)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-302-42

Query Match      2.2%; Score 30; DB 9; Length 1574;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1286 AAACAACGAAAAAAAAAAAAAAAAAAAA 1315
      1534 AAACAACGAAAAAAAAAAAAAAAAAAAA 1563

RESULT 7
US-10-311-455-1913/C
; Sequence 1913, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation Status of Genes
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1913
; LENGTH: 5898

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-311-455-1913

Query Match      2.2%; Score 30; DB 12; Length 5898;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1286 AAACAACGAAAAAAAAAAAAAAAAAAAA 1315
DB      2026 AAACAACGAAAAAAAAAAAAAAAAAAAA 1997

RESULT 9
US-10-239-676-179/C
; Sequence 179, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239,676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
; DE 10019058.8
; DE 10019173.8
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; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 179
; LENGTH: 5898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-239-676-179

Query Match
Best Local Similarity 100.0%; Score 30; DB 14; Length 5898;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
2026 AACCAACGAAAAAAAAAAAAAAAAAAAA 1997
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RESULT 10
US-10-311-455-1804/c
; Sequence 1804, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1804
; LENGTH: 6126
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-311-455-1804

Query Match
Best Local Similarity 100.0%; Score 30; DB 12; Length 6126;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
766 AACCAACGAAAAAAAAAAAAAAAAAAAA 737
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RESULT 11
US-10-311-455-1278/c
; Sequence 1278, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
```

```
; CURRENT APPLICATION NUMBER: US/10/311.455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1278
; LENGTH: 6154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-311-455-1278

Query Match
Best Local Similarity 100.0%; Score 30; DB 12; Length 6154;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
882 AACCAACGAAAAAAAAAAAAAAAAAAAA 853
```

```
RESULT 12
US-10-311-455-367/c
; Sequence 367, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 367
; LENGTH: 6510
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-311-455-367

Query Match
Best Local Similarity 100.0%; Score 30; DB 12; Length 6510;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
5115 AACCAACGAAAAAAAAAAAAAAAAAAAA 5086
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RESULT 13
US-10-027-632-174763
; Sequence 174763, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
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; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174763
; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2940917)
; OTHER INFORMATION: n = A,T,C or G
US-10-02-632-174763
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Query Match          2.2%; Score 30; DB 13; Length 2940917;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1286 AACACACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2677001 AACACACGAAAAAAAAAAAAAAAAAAAA 2677030
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RESULT 14
US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1250374
US-10-359-385-5
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Query Match          2.2%; Score 29; DB 12; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 484 ACCGTGTAGAGCGCGTAATAATCGAGT 512
DB 717 ACCGTGTAGAGCGCGTAATAATCGAGT 745
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RESULT 15
US-10-311-455-2039/C
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; Sequence 2039, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2039
; LENGTH: 4274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2039
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Query Match          2.2%; Score 29; DB 12; Length 4274;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 2102 AACGAAAAAAAAAAAAAAAAAAAAATTA 2074
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Search completed: September 25, 2003, 11:46:48
Job time : 334 secs
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352 CAATGTTGGCCATTTGGTAAATATTAGATGTTGAATTTATTTTAAATGAGCGCGC 411
1389 CAATGTTGGCATTTGGTAAATCTTAGATGTTGAATTTATTTAAATGAGCGAGC 1448
412 TCGAAGGATTTGGTTGTTGTAACCTTTCGAAATATGTCGGATGCGGACGAGGAG 471
1449 TCAAGGATTTGGTTGTTGTAACCTTTCGAAATATGTCGGATGCGGACGAGGAG 1508
472 AAATTCACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 531
1509 AAATTCACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 1568
532 GTGATGACTAATTAATAAGGCGGTGAACCCCTACAGGAATGCGTGAATTAATCACTT 591
1569 GTAATGACAAATTAATAAGGCGGTGAACCCCTACAGGAATGCGTGAATTAATCACTT 1628
592 GTGGGCGGCTCTACAGCCCGGACTTCTATGAGGAGCGGCTCTTGTCCAGGCAAC 651
1629 GTGGGCGGCTCTACAGCCCGGACTTCTATGAGGAGCGGCTCTTGTCCAGGCAAC 1688
652 CAGAGGAGTCTTCATGATGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACG 711
1689 CAGAGGAGTCTTCATGATGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACG 1748
712 GCGTTTCATATCGGCGCCCACTGCTGCAAGCTGATACCGAGGCGCTACCTTCGAGGC 771
1749 GCGTTTCATATCGGCGCCCACTGCTGCAAGCTGATACCGAGGCGCTACCTTCGAGGC 1808
772 GCGTTTCATATCGGCGCCCACTGCTGCAAGCTGATACCGAGGCGCTACCTTCGAGGC 831
1809 GCGTTTCATATCGGCGCCCACTGCTGCAAGCTGATACCGAGGCGCTACCTTCGAGGC 1868
832 TATGCGGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 891
1869 TATGCGGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 1926
892 GCTGATACCGGCTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGT 944
1927 GCTGATACCGGCTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGT 1986
945 -----CAGTTACGAGGAG 958
1987 CAGTTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACG 2046
959 TTTATGCTGCGAGCCCTACGACACGACGACGACGACGACGACGACGACGACGACG 1018
2047 TTTATGCTGCGAGCCCTACGACACGACGACGACGACGACGACGACGACGACGACG 2106
1019 CCATGATGCTTTGCGGCTTGAACGATGCGAAGACTAGAGGCGATGCTATGATGTTGG 1078
2107 CCATGATGCTTTGCGGCTTGAACGATGCGAAGACTAGAGGCGATGCTATGATGTTGG 2166
1079 GTCGCTCTTCTTCATTTGCGAGGCTATATATACCAAGGAGGAGTACCAACGTTTGGTC 1138
2167 GTCGCTCTTCTTCATTTGCGAGGCTATATATACCAAGGAGGAGTACCAACGTTTGGTC 2226
1139 CATATTAATGATAAACCATTAAACAACAACAACAACAACAACAACAACAACAACA 1198
2227 CATATTAATGATAAACCATTAAACAACAACAACAACAACAACAACAACAACAACA 2250
1199 CAACCTTCATTTGCGGAG 1258
2251 -AACCTTCATTTGCGGAG 2309
1259 GTAGACATCACTTTAGCACTCAAGAAACAACAACAACAACAACAACAACAACAACA 1318
2310 GTAGACATCACTTTAGCACTTTAAACAAAAAATGCAAAAAAATGCAAAAAAATG 2369

RESULT 2
US-09-176-657-5
; Sequence 5, Application US/09176657

Patent No. 6020164
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guebler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 1250374
US-09-176-657-5
Query Match 20.6%; Score 275.6; DB 3; Length 1506;
Best Local Similarity 60.2%; Pred. No. 1.5e-68;
Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7;
222 GACAGATGATGCGCGCCCGGACGAGCGGCGAGC---CCGAGACAGAACCTTGTGAACAC 278
452 GACAGAGGTGAGACACAGACAGAGCGGCGAGTCAAGACACAAATAGTGAATATTC 511
279 AGAAACAAAGTCCCAAGCCCAAGCGGCTGATGTGTCACATCTCCCTTCGCGGGA 338
512 AGAGAGTAAATCTACCCGGAACGCGTCAATGCTTAATATTCCTTCGCGGGA 571
339 TCCAGACCTCGACAAATGTTTGGCAATTTGGTAAATATTAGATGTTGAATATTTT 398
572 CCTGACCTCCGCGAGATGTTTGGGCACTTTGGCAATCTAGATGAGAAATATCTT 631
399 TAATGAGGCGGCTGGAAGGATTTGTTGCTAACTTTCGAAATAGTGGGATGCGGA 458
632 TAATGAGGCGGCTGGAAGGATTTGTTGCTAACTTTCGAAATAGTGGGATGCGGA 491
459 CAGGCGGAGGAGAAATGCAAGGATGCTGATGAGGCGGCTAAATGAGGATTAATA 518
632 CAGGCGGAGGAGAAATGCAAGGATGCTGATGAGGCGGCTAAATGAGGATTAATA 751
519 TCGACAGCAGCGGCTGATGATTAATAAAGGCGTGAACCCCTACACCAATGCTGGA 578
752 TCGTACAGCAGGATGATTAATAAAGGCGTGAACCCCTACACCAATGCTGGA 811
579 ATTAATGCAAGTGTGGGCGGCTGATGAGGCGGCTGATGAGGCGGCTGATGAGG 628
812 ATTAATGCAAGTGTGGGCGGCTGATGAGGCGGCTGATGAGGCGGCTGATGAGG 871
629 CCGGCTGCTGCTGCGAGGCGGCAACGAGGATGCTTCATGTA--CACTGGGCCCAAGTTC 686
872 AGCAGATGTGCTCAGGCGCAATGATGACAGAGTGCCTCTATCAGGAAGAGGCGATCAA 931
687 ACTGTATATATCTTGTGCAATGCTGCTGCTTTCATA--TCGGGCGGCGATGCTGAGC 743
932 CACTTACATTCCTTTAATCATCTCCGCGCTTCCCTTACCTACTGAGGCGACAGCGGCG 991
744 TGCATACGAGGAGGCTCACTTTCGAGGCGGCTGATGAGGCGGCTGATGAGGCGG 803
992 CGCTTTCAGAGGAGCCATTGAGGCGGCGAGAGGCGGCGGAGTATATGTCAGTCCGA-- 1049
804 TCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 863
1050 -GCGGTACCTCCAAAGGCAATCCCGCTATTCAGGAGGCGGCGGCGGCGGCGGCGG 1104
864 TGCAATTAATTTGCTAGGAGGTTGATGCTGATACGCTACGAGCGGCGGCGGCGGCGG 923
1105 -----ATATGCAAGCGCTGCTACTGCAACCGCAGCGGCTGCTGAGC 1149

QY	924	TACGTGCTGCTGCTACAGTGTGACATTTACAGCAGAGTTTATCTGTGCGACCCCTTACACACA	983
Db	1150	CGCTGCACACCCCTTACAGTGTGAGGTTTAAAGCAGGGTGTACACACCCGACCCCTTACCAATGC	1209
QY	984	CACACTTGTCTCCAGGCCCCACCTTACAGGGCGTTGTGTGCCATGTATGCTTTTGGCGCCCTTGAC	1043
Db	1210	C---CTTCCGCCCTGTGCTGTACCTATTGGAGTTTGGCGCTGTGGCGAGTTTATACCGAGGTGG	1266
QY	1044	CGATGCCAAGACTAGAGACCATGCTGATGATGTGGGTCTCGTTCTTCTTATTATTCAGAGC	1103
Db	1267	CTACAGCCGATTTGCCCCCTACTAGAAAGTACGTAGACCCCTGGCAATGTGGACAGCCCC	1326
QY	1104	TAGTATATATCCAAAGGGGGATCAACAACCGTTTGGCTCCATATTAAATGATTTAAACCATTTAAA	1163
Db	1337	CAGTTTCATGAGGCCCTGGCTATTGCAATATTACTAGTAGAGGAACTCTATTGCAAGAATGA	1386
QY	1164	CAACACAGCAAAAAACAAAAACAAAAACAAAAACCAA	1201
Db	1387	AGAGCAAAACCAAAACAAACCAAAACCAAAACCAAA	1424

RESULT 3

```

US-09-421-299-5
: Sequence 5, Application US/09421299
: Patent No. 6524579
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Alina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/09/421,299
: CURRENT FILING DATE: 1999-10-20
: EARLIER APPLICATION NUMBER: 09/176,657
: EARLIER FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
US-09-421-299-5

```

Query Match	20.68;	Score 275.6;	DB 4;	Length 1506;
-------------	--------	--------------	-------	--------------

Best Local Similarity 60.2%; Pred. No. 1.5e-68;
Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7.

[illegible]

OY	519	TGCGAAGACGGCGATGACTAAATAAAAAGCCGTGAACCCCTTACCACATGGCTGGA	578
Dd	752	TGCTACACGACGTGTAATGACCAATTAAACAATGTGTACACCATTATGCCAATGGTTGGA	811
OY	579	ATTAAATTCAGTTGTGGCGGGGTCTACAGCCCCGACTTCTATGCAG-----GCA	628
Dd	812	ATTAAAGCCAGTAGTTGGAGCTGTATATATGTCCGGAGTTATATGACGATCAGCTTTC	871
OY	629	CGGTGCTGTGTGGCAGGGCCAACGAGGGGATCTTCCATGTA--CATGGCCCCAGTTC	686
Dd	872	AGCAGATGTGTCCCTAGGCAATGATGCGAGTGCCCTATACGAMAAGGGGGTATCAA	931
OY	687	ACTGTATATATCTTCTGCAATGCCGTGGCTTTCACATA---TCGGCGCCGACTGTGCGAGC	743
Dd	932	CACHTAACCTTCCTTAATCATCTCTGGCTTCCCTTAACCTACTGTGAGCACACAGCGGAGC	991
OY	744	TGCATACCAGGGGCTCACCCTTCGAGGCCGTGTGTGCAACCGTGTACAAACCTTCAGAGC	803
Dd	992	CGCTTTGAGAAGAACCCCTTTGAGGGGGCAGAGGGCGGCACTAATATGTGTGCAGTCCGA--	1049
OY	804	TGCGGCGCCCCACCCCACATCCGGGCTATGGCGGAGTAGTGTATCAAGAGCCAGTSTA	863
Dd	1050	-GGGTACTTCCAAACAGCATGCCCGCTTATCCAGGGGTGGATATGCAAGCTTACAG-----	1104
OY	864	TGGCAATTAATTTGTACAGGGTGTTCAGCTGCATACCGCTACGGCCAGCCACCCTTCGC	923
Dd	1105	-----ATATGCAACAGCCTGTCTACTGCACCAACCACGACCAACCGCTGTGCGAGC	1149
OY	924	CAGTGTGCTGCTACAGGTGACATTCACGAGCGAGTTATGTGCTCGGACCCCTACACACA	983
Dd	1150	CGCTGCACGCCCTTACATGCTGAGGTTATGAGCAGGGTGTACAGACGCGACCCCTTACATGCG	1209
OY	984	CACACTTGCTCAGCCCCCACCTCAGCGCGTGTGATGCCAATGATGCTTTTGGCCCTTGAC	1043
Dd	1210	C---CTTGCCCCCTCCGCTACTATTTAGGAGTTGGCGCTGTGCGAGTTATACCGAGTGG	1266
OY	1044	CGATGCCAAGACTAGAGCCCATGCTGATGATGTGGTCTGCTTCTTCTTATTCAGAGC	1103
Dd	1267	CTAAGCGCGATTTGCCCTCTACTGATGAGCTGAGACCCCTGCMAATGGAGACAGCCCC	1328
OY	1104	TAGTATATATACCAAGGGGATCAACACCGTTTGGCTCTCATATTAAATGATAAACCATTTAA	1163
Dd	1327	CAGTTTCATGAGCGCTGGCTATTGCAATTTTACTAGTGTAGAGGAACCTATATGCAAGATGA	1386
OY	1164	CAAAACAAGCAAAAAACAACAAAAACAACAAAAACCA	1201
Dd	1387	AGAGGAAAAACAACCAACCAACCAACCAACCAAA	1424

RESULT

US-09-014-969-14
Sequence 16-14, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racle, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:

Query Match 3.7%; Score 50; DB 1; Length 7218;
Best Local Similarity 7.5%; Pred. No. 0.0007;
Matches 17; Conservative 132; Mismatches 77; Indels 0; Gaps 0;

[illegible]

RESULT 6
 US-08-628-417-6
 : Sequence 6, Application US/08628417
 : Patent No. 5627054
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: GILLESPIE, DAVID
 : TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
 : TITLE OF INVENTION: POLYMERASE CHAIN REACTION
 : NUMBER OF SEQUENCES: 7
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
 : ADDRESS: DEFENSE COMMAND
 : STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
 : CITY: ABERDEEN PROVING GROUND
 : STATE: MARYLAND
 : COUNTRY: USA
 : ZIP: 21010-5423
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/628,417
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BIRFOUT, ULYSSES J
 : REGISTRATION NUMBER: 39,908
 : REFERENCE/DOCKET NUMBER: DAM 398-94
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 410-671-1158

US-09-271-815-3
; Sequence 3, Application US/09271815
; Patent No. 6297036
; GENERAL INFORMATION:
; APPLICANT: BERGSMÄ, DERK
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
; FILE REFERENCE: GH-70172-1
; CURRENT APPLICATION NUMBER: US/09/271,815
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 09/027,064
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/053,924
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
-09-271-815-3

Query Match 3.4%; Score 45.2; DB 3; Length 1338;
Best Local Similarity 47.8%; Pred. No. 0.0062;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGCGCCCTGACACATGCTCAGCTTATGCTTCGCGAGTTCGCTCCACCCAGAAAT 62
DB 686 GGTGCGTCCATACCAACCTTCACACACCCCGAGCTGATGATGAGCTGGTG 745
QY 63 GGATCTCTGACAAATACAGGCGCTCATCCCATC GCGCGCAGAGACAGCGCCAGCC 122
DB 746 GCGGCGCTGCTACTGCTCCACCTGACACCGCGTGGCCCGCCAGCAGCGGCTGCT 805
QY 123 CACTGTCGCCGACACATTAATGATCTCTCTACAGACAGCGACCTGAGAGAGCG 182
DB 806 CAGCCCTCGGAGCTGAGTGAAGTGTCTCCACCGCTCCGCTCTGATGACCTG 865
QY 183 CTATATACAGCGCAGACGCGTCTCGGACCGCCAGAGAGAGATGATCGCCCGAC 242
DB 866 CCACTCTGGGGCTCACTGCGCTCCGTGTTACCCGAGACAGCAGCAGCAGCTCGTG 925
QY 243 CGACGGCCAGCCCGACACAACTTCTGAAGC 270
DB 926 ACCCTGCCCTCTGCGGGGCGCTCTGAAGC 959

RESULT 10

-09-027-064-1
; Sequence 1, Application US/09027064
; Patent No. 6133006

; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: BERGSMÄ, DERK
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASE-HTLAR33
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,064
; FILING DATE: 20-FEB-1998
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,924
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE NUMBER: GH-70172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-027-064-1

Query Match 3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGCGCCCTGACACATGCTCAGCTTATGCTTCGCGAGTTCGCTCCACCCAGAAAT 62
DB 1742 GGTGCGTCCATACCAACCTTCACACACCCCGAGCTGATGATGAGCTGGTG 1801
QY 63 GGATCTCTGACAAATACAGGCGCTCATCCCATC GCGCGCAGAGACAGCGCCAGCC 122
DB 1802 GCGGCGCTGCTACTGCTCCACCTGACACCGCGCTGCGCCCGACAGCAGCGGCTGCT 1861
QY 123 CACTGTCGCCGACACATTAATGATCTCTCTACAGACAGCGACCTGAGAGAGCG 182
DB 1862 CAGCCCTCGGAGCTGAGTGAAGTGTCTCCACCGCTCCGCTCTGATGACCTG 1921
QY 183 CTATATACAGCGCAGACGCGTCTCGGACCGCCAGAGAGAGATGATCGCCCGAC 242
DB 1922 CCACTCTGGGGCTCACTGCGCTCCGTGTTACCCGAGACAGCAGCAGCAGCTCGTG 1981
QY 243 CGACGGCCAGCCCGACACAACTTCTGAAGC 276
DB 1982 ACCCTGCCCTCTGCGGGGCGCTCTGAAGC 2015

RESULT 11

US-09-271-815-1
; Sequence 1, Application US/09271815
; Patent No. 6297036

; GENERAL INFORMATION:
; APPLICANT: BERGSMÄ, DERK
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
; FILE REFERENCE: GH-70172-1
; CURRENT APPLICATION NUMBER: US/09/271,815
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 09/027,064
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/053,924
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-271-815-1

Query Match 3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGCGCCCTGACACATGCTCAGCTTATGCTTCGCGAGTTCGCTCCACCCAGAAAT 62

Db 1742 GGTGTGCTCCATCAACCACTTCAACACACCCCGAGCTGATGATGAGCTGTG 1801
QY 63 GGCAATCTCGAGATATACAGGGCCCTCATCCCATCCCGGCGCAGACACCGCCAGCC 122
Db 1802 GGGCGGCTGCTGACTGTCTCCACCTCAACCGAGCGCCCGCCAGCAGCCGCTGCT 1861
QY 123 CACGTGCCCCCGCACATTAATTAATCTCTCTACACAGAGCAGCTGAGAGAGAGC 182
Db 1862 CAGCCCTCCGAGCTCGATGATGATGATGATGATGATGATGATGATGATGATG 1921
QY 183 CTATACAGAGCAGAGCGCTCTCCGACCCGACAGACAGATGATGATGATGATG 242
Db 1922 CCACCTGAGGAGCTGACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1981
QY 243 CGAGGCGCAGCCCGACAGACACCTTCTGAAAAC 276
Db 1982 ACCCTGCCCCCTCCCTGAGGCGCCCTCTGAAAAGC 2015

RESULT 12

S-08-676-967-2
: Sequence 2, Application US/08676967
: Patent No. 5747317
: GENERAL INFORMATION:
: APPLICANT: COLLINS, KATHLEEN
: TITLE OF INVENTION: Human Telomerase
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Science & Technology Law Group
: STREET: 268 Bush Street, Suite 3200
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/676,967
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman Ph.D., Richard A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UCB96-055
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)343-4341
: TELEFAX: (415)343-4342
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2277 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-676-967-2

Query Match 3.4%; Score 45; DB 1; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;

Matches 109; Conservatve 46; Mismatches 178; Indels 3; Gaps 1;

QY 215 CCACAGACAGATGATGCGCCCGGACGCGCAGCCCGCAGACACAACTTCTGAAA 274
Db 257 CNAARGAARAAAGGNAARAAAGARAAAYWSNGARTGCCNAARAGARCCNAARACNAARA 316
QY 275 ACACAGAAACAACTCCAGCCGAGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 334
Db 317 ARGCGAARAGTNGCGAATGAARARACNGMNTNATHATGMAAAYTTWMSNTTAAATGTYM 376
QY 335 GGATCCAGACCTCCGACAAATGTTGGCCAAATTTGTAATTTAGATGTTGAATTA 394

Db 377 SNGARGAAYGAYTNAARACNGTNTTGGCNCARTTGGGNGCNGTNTGACRGTNAAYATHC 436
QY 395 TTTTAA---TGACGGGGGCTCCGAAAGGATTTGGTTTCTTACTTTGCAAAATATGTCGG 451
Db 437 CNGMNAARCCGAGAGNAARATGNGNGNTTGGTNTTGGTNTTGGTNTTGGTNTTGGTNTT 496
QY 452 ATGGGAGAGGGGAGGAGAGAAATGACAGCTTACCGTGTGAGGCGCGTAAATTCGAGG 511
Db 497 ARGCGAARAGCAYTNAARAGNATGATGATGATGATGATGATGATGATGATGATG 556
QY 512 TTAATTAATGCGACAGACGCGCTGATGATGATGATGATGATGATGATGATGATG 547
Db 557 TNGAYTGGCGMGTGNAARAGATTAATTAARAGAYA 592

RESULT 13
US-08-676-974-2
: Sequence 2, Application US/08676974
: Patent No. 5770422

: GENERAL INFORMATION:
: APPLICANT: COLLINS, KATHLEEN
: TITLE OF INVENTION: Human Telomerase
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Science & Technology Law Group
: STREET: 268 Bush Street, Suite 3200
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/676,974
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman Ph.D., Richard A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UCB96-055
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)343-4341
: TELEFAX: (415)343-4342
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2277 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-676-974-2

Query Match 3.4%; Score 45; DB 1; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;

Matches 109; Conservatve 46; Mismatches 178; Indels 3; Gaps 1;

QY 215 CCACAGACAGATGATGCGCCCGGACGCGCAGCCCGCAGACACAACTTCTGAAA 274
Db 257 CNAARGAARAAAGGNAARAAAGARAAAYWSNGARTGCCNAARAGARCCNAARACNAARA 316
QY 275 ACACAGAAACAACTCCAGCCGAGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 334
Db 317 ARGCGAARAGTNGCGAATGAARARACNGMNTNATHATGMAAAYTTWMSNTTAAATGTYM 376
QY 335 GGATCCAGACCTCCGACAAATGTTGGCCAAATTTGTAATTTAGATGTTGAATTA 394
Db 377 SNGARGAAYGAYTNAARAGNATGATGATGATGATGATGATGATGATGATGATG 436
QY 395 TTTTAA---TGACGGGGGCTCCGAAAGGATTTGGTTTCTTACTTGAATTAATGTCGG 451

DB 437 CMMGNAARCCNGAYGNARATGMCNGCTTGGTTCATTCARTTYAARAAYTNTNG 496
QY 452 ATGCGAGAGGGCGAGGGAATTCACCGTACGGTGTAGAGGCGCTAAATCGAG 511
DB 497 AFGCGNNAARCCNTTNAARGNATGAATGAARATTAARGNMGNGCTNGCNG 556
QY 512 TTAATTAATGCGACGACCGGTGATGACTAATAA 547
DB 557 TNGAYTGGCGCTGCTGCGNNAARGAAYAAATTAARGAVA 592

RESULT 14
US-09-098-487-2
; Sequence 2, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, Kathleen
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,487
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-098-487-2

Query Match 3.4%; Score 45; DB 2; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

QY 215 CCACACAGACAGATGATGCGCCCGACGCGCGACGCGCCAGACACAACTTGTGAA 274
DB 257 CNAARGAARAARCAARAYGAARAYWMSGARTRGCCNNAARARARCCNNAARCA 316
QY 275 ACACAGAAAACAGTCCCGACGCCAGCGCTCATGTGTCCAACTCCCTCCGCTTCC 334
DB 317 AAGCNAARCTGCGCAGAAAGCGCGCTCATGTGTCCAACTCCCTCCGCTTCC 376
QY 335 GGGATCCAGACCTCCGACAAATGTTGGCAATTTGTAATAATATTAGATTGAATTA 394
DB 377 SNGARGATGATTTNARACNGTNTTTCATTTGGGCGCTGTTNGARGTNAATATTC 436
QY 395 TTTTAA--TGAGCGGGGCTCGAAGGATTTGTTTCTTAATCTTGCAGAAATAGTGGC 451
DB 437 CMMGNAARCCNGAYGNARATGMCNGCTTGGTTCATTCARTTYAARAAYTNTNG 496
QY 452 ATGCGAGAGGGCGAGGGAATTCACCGTACGGTGTAGAGGCGCTAAATCGAGG 511

DB 497 AFGCGNNAARCCNTTNAARGNATGAAYATGAARATTAARGNMGNGCTNGCNG 556
QY 512 TTAATTAATGCGACGACCGGTGATGACTAATAA 547
DB 557 TNGAYTGGCGCTGCTGCGNNAARGAAYAAATTAARGAVA 592

RESULT 15
US-09-620-312D-1019
; Sequence 1019, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungting
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhilwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PL_FL_genes Version 1.0
; SEQ ID NO 1019:
; LENGTH: 1477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(753)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1477)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-1019

Query Match 3.3%; Score 44.8; DB 4; Length 1477;
Best Local Similarity 52.0%; Pred. No. 0.0085;
Matches 128; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 295 CCCAAGCGGCTGATGTCGCAACATCCCTCCGCTCCGGATCCGAGTCAGACGACAA 354
DB 442 CCAATGCGCTCTATGTGGGTCCCTGCACTTCATATACATGAGACATGCTCCGGG 501
QY 355 ATGTTTGGCAATTTGTAATAATATTAGATTGTAATAAT--TTTAATGAGCGG 408
DB 502 ACTTTGAGCCCTTTGTAATAATTTGATATTGTCCTGATGAAGACTACATACAGGC 561
QY 409 GCGTCGAAGGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 468
DB 562 CCGCTTAAGGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 621
QY 469 GAGAATTCACGAGTACGCTGTGAGAGGCGCTTAATCGAGTAAATTAATGCGACGA 528
DB 622 GAACAGTTGAATGCTTTGAGCTTCTGCTGACCTATGAGAGGCTTGGCCATGTGAG 681

QY	529	CGCGTG	534
	11	11	
Db	682	CGACTG	687

Search completed: September 25, 2003, 11:39:25
Job time : 90 secs

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OY 592 GTGGGCGGGTCTACAGCCCGGACCTTCTATGACAGGCGGTGTGTGTCAGAGCCAC 651
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Db 1629 GTGGGTGACGTCTACAGTCCGGAATCTATGACAGGCGGTCTGTGTGTCAGAGCCAC 1688
OY 652 CAGAGGAGATCTTCCATGTCAGTGGCCCACTTCACTGTATATCTTGTGCANGCCT 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1689 CAGAGGAGATCTTCCATGTCAGTGGCCCACTTCACTGTATATCTTGTGCANGCCT 1748
OY 712 GGGCTTCATATCGGGCGGCGGACGTGTGACAGGAGGCGGTCTGCTCCGAGGC 771
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Db 1749 GGGCTTCATATCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1808
OY 772 CGTGTGTCAGCGGTGTACAAACACCTTTCAGAGCTGCGGCGGCGGCGGCGGCGGCGG 831
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1809 CGGCGTGCACCGGTGTACAAACACCTTTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1868
OY 832 TATGGCGAGTACTGTATCAAGAGCCAGTGTATGGCAATTAATTTGTACAGGGTGTAC 891
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1869 TACGGCGGTGTGTATAC--CAGGATGATTTATATGTGTGACAGATTTATGTGTGTAT 1926
OY 892 GCTGATACCGGTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 944
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1927 GCTGATACCGGTGTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1986
OY 945 -----CAGTTAGGAGAG 958
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1987 CAGTTAGTCTTCTGTGACGAGATGAAATTTCTGTACACCTCTGACAGTTAGGAGAG 2046
OY 959 TTTATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1018
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Db 2047 TTTATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2106
OY 1019 CCATGATGCTTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1078
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Db 2107 CCATGATGCTTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2166
OY 1079 GTCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1138
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Db 2167 GTCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2226
OY 1139 CATATTAAATGATTAACCACTTAACCAACAGCAACCAACCAACCAACCAACCAACCA 1198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2227 CATATTAAATGATTAACCACTTAACCAACAGCAACCAACCAACCAACCAACCAACCA 2250
OY 1199 CAACCTTCATGTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2251 -AACCTTCATGTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2309
OY 1259 GTAGGAGATCATTGTAGCAACTCAAGCAACAGCAACAGCAACAGCAACAGCAACAGCA 1318
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2310 GTAGGAGATCATTGTAGCAACTTTTAAAAAATCAAAAAAATCAAAAAAATCAAAAAA 2369

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; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1250374
US-10-359-385-5

Query Match
Best Local Similarity 60.2%; Pred. No. 1.3e-67;
Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7;

OY 222 GACAGATGATCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 278
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Db 452 GACAGAGAGTGTGAGACAGACAGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 511
OY 279 AGAAGAGATCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 512 AGAAGAGATCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 571
OY 339 TCCAGACCTCCGCAAAATGTTTGGCAATTTGTGTAATAATTAATTAATTAATTAATTT 398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 572 CCTGACCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 631
OY 399 TAATGAGCGGGGCTCGAAGGAGATTTGGTTTCTGTAACCTTTGAAATAGTGGAGTGGGA 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 TAATGAGCGGGGCTCGAAGGAGATTTGGTTTCTGTAACCTTTGAAATAGTGGAGTGGGA 691
OY 459 CAGGCGGAGGAGAAATGTCAGCGGTACCGGTGTAGAGGCGGCGGCGGCGGCGGCGGCGG 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 CAGGCGGAGGAGAAATTAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 751
OY 519 TGCAGACGACGCGGTGTGATTAATAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 752 TGCATACGACGCGGTGTGATTAATAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 811
OY 579 ATTAATCAAGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 628
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 812 ATTAAGCGCGGTGTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 871
OY 629 CGGTGCTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 686
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 872 AGGAGATGTGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 931
OY 687 ACTGTATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 743
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 932 CACTTACATCTCTTATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 991
OY 744 TGCATACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 803
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 992 CGCTTTCAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1049
OY 804 TGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 863
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1050 -GGGTAACCTTCAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1104
OY 864 TGGCAATTAATTTCTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 923
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1105 -----ATATGACAGCGCTGTACTGCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1149
OY 924 CACTGCTGTGCTTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 983
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1150 CGCTGCGAGCGGCTTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1209
OY 984 CACACTGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1043
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1210 C---CTTGCCCTTGCCGCTAGCTATGAGTGGCGGCTGTGGCGAGTTTATACGAGGTGG 1266
OY 1044 CGATGCCAAGACTAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1267 CTACAGCGGATTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1326
OY 1104 TAGTATATACCAAGGGGATCAACCGTTTGTCTCCATTAATTAATTAATTAATTAATTA 1163
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RESULT 3
US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5

```


US-09-864-761-11804

Query Match 9.2%; Score 123.8; DB 9; Length 473;
Best Local Similarity 91.6%; Pred. No. 9,4e-25;
Matches 11; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 220 CAGACAGATGATCCGCCCGCCAGCCGACCCCAACACACAACTTCTGAAACACA 279
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DB 269 CAGACAGATGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 328
QY 280 GAAACAGCTCCAGCCGACGAGGCTGATGTGTCCACATCCCTTCGGTTCCGGGAT 339
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 329 GAAACAGCTCCAGCCGACGAGGCTGATGTGTCCACATCCCTTCGGTTCCGGGAT 388

QY 340 CCAGACCTCCGACCAATGTTGG 362
DB 389 CCGAGCTCCGACCAATGTTGG 411

RESULT 6

US-09-864-761-28375
Sequence 28375, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 28375
LENGTH: 125

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: MAP TO AC006075.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
OTHER INFORMATION: EST_HUMAN HIT: 225303.1, EVALUE 9.00e-61
OTHER INFORMATION: NT HIT: 911431054, EVALUE 2.00e-64
OTHER INFORMATION: SWISSPROT HIT: P54537, EVALUE 1.40e-00
US-09-864-761-28375

Query Match 8.2%; Score 109.6; DB 9; Length 125;
Best Local Similarity 92.7%; Pred. No. 4.7e-21;
Matches 11; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 239 CGACGAGCGCCAGCCCGCCAGACACAACTTCTGAAACACAGAAACAGTCCAGCCCA 298
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DB 1 CGACGAGTGGCCAGCCCGCCAGACACAACTTCTGAAACAGAAACAGTCTCAGCCCA 60
QY 299 ACGGCTGATGTGTCCAAATCCCTTCGGTTCCGGATCCAGACCTCCGACAAATGT 358
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DB 61 ACGGCTGATGTGTCCAAATATCCCTTCAGGTTCCGGATCCGACCTCAGACAAATGT 120

QY 359 TTGG 362
DB 121 TTGG 124

RESULT 7

US-09-864-761-22653
Sequence 22653, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABUGATANI, HIROKUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT FILING DATE: 2002-12-18
CURRENT APPLICATION NUMBER: US/10/017,161
PRIORITY FILING DATE: 2001-06-18
PRIORITY APPLICATION NUMBER: JP 2001/246789
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2191
LENGTH: 2350
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(2350)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2150)
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (7)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (9)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (13)..(15)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (17)..(18)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (20)..(21)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (23)..(24)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (31)
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NAME/KEY: modified_base
LOCATION: (34)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (39)
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NAME/KEY: modified_base
LOCATION: (41)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (49)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (51)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:

NAME/KEY: modified_base
LOCATION: (71)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (90)
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FEATURE:
NAME/KEY: modified_base
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NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (106)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (109)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (111)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (113)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (170)..(171)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (195)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (197)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (209)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 25, 2003, 11:55:10 : Search time 27 Seconds
(without alignments)
1137.605 Million cell updates/sec

Title: US-09-809-545A-2
Perfect score: 1086
Sequence: 1 MTNKKAVNPYTNCKMLNPVY.....VLSSLDASTYGGYNRFAPY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters: 566894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications-AA:*

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10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1086	100.0	203	10 US-09-809-545A-2	Sequence 2, Appl1
2	351	50.7	330	9 US-09-794-591-2	Sequence 2, Appl1
3	288	26.5	366	12 US-10-359-385-2	Sequence 2, Appl1
4	116	10.7	3063	12 US-10-301-822-26	Sequence 26, Appl1
5	116	10.7	3063	12 US-10-177-293-61	Sequence 61, Appl1
6	116	10.7	3063	12 US-10-177-293-63	Sequence 63, Appl1
7	96	8.8	388	12 US-10-012-952A-172	Sequence 172, Appl1
8	96	8.8	760	8 US-08-754-311B-2	Sequence 2, Appl1
9	93	8.6	692	15 US-10-156-761-14649	Sequence 14649, A
10	92.5	8.5	919	15 US-10-128-714-8387	Sequence 8387, Ap
11	90.5	8.3	481	15 US-10-156-761-112012	Sequence 12012, A
12	89.5	8.2	342	15 US-10-156-761-11221	Sequence 11221, A
13	88.5	8.1	363	15 US-10-156-761-10205	Sequence 10205, A
14	88	8.1	380	15 US-10-156-761-11952	Sequence 11952, A
15	88	8.1	2116	12 US-10-224-999A-3475	Sequence 3475, Ap

16	87.5	8.1	620	15 US-10-156-761-7979	Sequence 7979, Ap
17	87	8.0	465	15 US-10-205-823-136	Sequence 136, App
18	86.5	8.0	262	10 US-09-263-689-14	Sequence 14, Appl
19	86.5	8.0	262	15 US-10-235-674-14	Sequence 14, Appl
20	86.5	8.0	742	15 US-10-156-761-12153	Sequence 12153, A
21	86	7.9	245	9 US-09-796-858-20	Sequence 20, Appl
22	86	7.9	275	12 US-10-313-833-3	Sequence 3, Appl1
23	86	7.9	279	11 US-09-813-408-21	Sequence 21, Appl
24	86	7.9	337	15 US-10-156-761-12003	Sequence 12003, A
25	86	7.9	550	15 US-10-156-761-11905	Sequence 11905, A
26	85	7.8	275	8 US-08-322-678-7	Sequence 7, Appl1
27	85	7.8	275	9 US-09-060-854B-3	Sequence 3, Appl1
28	85	7.8	275	10 US-09-976-414-7	Sequence 7, Appl1
29	85	7.8	275	10 US-10-324-152-1	Sequence 1, Appl1
30	85	7.8	275	12 US-09-824-607-1	Sequence 1, Appl1
31	85	7.8	275	12 US-10-242-549-4	Sequence 4, Appl1
32	85	7.8	275	14 US-10-075-907-2	Sequence 2, Appl1
33	85	7.8	275	14 US-10-075-895-2	Sequence 2, Appl1
34	85	7.8	275	15 US-10-033-325-3	Sequence 3, Appl1
35	85	7.8	275	15 US-10-228-572-3	Sequence 3, Appl1
36	85	7.8	308	15 US-10-156-761-13336	Sequence 13336, A
37	85	7.8	382	14 US-10-090-624-31	Sequence 31, Appl
38	85	7.8	382	15 US-10-033-325-2	Sequence 2, Appl1
39	85	7.8	382	15 US-10-104-693-2	Sequence 2, Appl1
40	85	7.8	382	15 US-10-228-572-2	Sequence 2, Appl1
41	84.5	7.8	623	15 US-10-156-761-11120	Sequence 11120, A
42	84	7.7	146	15 US-10-156-761-8967	Sequence 8967, Ap
43	84	7.7	275	11 US-09-813-408-18	Sequence 18, Appl
44	83.5	7.7	485	10 US-09-925-300-1664	Sequence 1664, Ap
45	83.5	7.7	584	15 US-10-156-761-12405	Sequence 12405, A

ALIGNMENTS

RESULT 1
US-09-809-545A-2
; Sequence 2, Application US/09809545A
; Patent No. US2002010804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-809-545A-2

Query Match 100.0%; Score 1086; DB 10; Length 203;
Best Local Similarity 100.0%; Pred. No. 9; 7e-99;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTNKKAVNPYTNCKMLNPVYGA	VSDFPAGTVLLCOANDESSMTSGPSSLYTSAMPG	60
DB	1	MTNKKAVNPYTNCKMLNPVYGA	VSDFPAGTVLLCOANDESSMTSGPSSLYTSAMPG	60
QY	61	FPYPATTAAGYGAHLRGRGRTVY	TFPRAAPPPPIPAVGGVYOEPPYGNKLLGGYA	120
DB	61	FPYPATTAAGYGAHLRGRGRTVY	TFPRAAPPPPIPAVGGVYOEPPYGNKLLGGYA	120
QY	121	AVRYAQPPTATAAAYS	SDSYGRVYAADPYHHTLAPATYGVGANNAPPLTDATRS	180
DB	121	AVRYAQPPTATAAAYS	SDSYGRVYAADPYHHTLAPATYGVGANNAPPLTDATRS	180
QY	181	VGLVLSLDASTYGGYNRFAPY	203	
DB	181	VGLVLSLDASTYGGYNRFAPY	203	

RESULT 2
US-09-794-591-2
; Sequence 2, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Shidara, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/145,391
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-591-2

Query Match 50.7%; Score 551; DB 9; Length 330;
Best Local Similarity 97.1%; Pred. No. 5,5e-46;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 16 MTNKAANPYTNGMKLNPNVGAIVSPDFYAGTVLLCOANOGSSMYSGPSSLVYTSAMPG 60
QY 61 PPYPATAAAAYRGAHLRGRTVYNTFRRAAPPPPIPAYGCVVY 105
DB 236 PPYPATAAAAYRGAHLRGRTVYNTFRRAAPPPPIPAYGCVVY 300

RESULT 3
US-10-359-385-2
; Sequence 2, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guejler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-2

Query Match 26.5%; Score 288; DB 12; Length 366;
Best Local Similarity 48.9%; Pred. No. 4e-20;
Matches 68; Conservative 11; Mismatches 54; Indels 6; Gaps 4;
QY 1 MTNKAANPYTNGMKLNPNVGAIVSPDFYAGTVLLCOANOGSSMYSGPSSLVYTSAMPG 56
DB 190 MTNKAANPYTNGMKLNPNVGAIVSPDFYAGTVLLCOANOGSSMYSGPSSLVYTSAMPG 249
QY 57 AMPGPPY-AAATAAAAYRGAHLRGRTVYNTFRRAAPPPPIPAYGCVVYDEPYGNKLL 115

Db 250 IIPGFPYPTAATTAAFRAHNRGRRTYGAVR-AVPEPTAPAYGVDMOPTDMHSLLL 308
QY 116 OCGYAARYAOPTPADAAA 134
DB 309 QPOPPLLOPLPLTYVWMA 327

RESULT 4
US-10-301-822-26
; Sequence 26, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-26

Query Match 10.7%; Score 116; DB 12; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.043;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;
QY 50 SLVYTSAMPGEPPYATAAAAYR-GAHLRGRTV-----YNTFRRAA 92
DB 2078 NNVIQPLQOPRPR-KIVIAVYEDGCHLGNRRTYGLPPONHISDEYTFRRSW 2136
QY 93 PPPPIPAYGVVYDEPYGNKLLQ--GGYAARYAOPTPADAAVSDSYGRVYAADPYH 149
DB 2137 DPSPSPVLGYKIVKYPGVSNEPMEAFVGEKMTSYTL----- 2171
QY 150 HTLAPAPTYGCAAMAFA-----PLTDAKTRSHADVGLVLSLQASTYOGGYNRF 200
DB 2172 HNLNPSTYIDV--NVYAQYDSGLSVPLTDGTT-----LYLNVTDLKTQIGMDTF 2220

RESULT 5
US-10-177-293-61
; Sequence 61, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatf, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Ganavarapu, Manjula
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian

```
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Best Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puzsatic, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul B.
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 61
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-61
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Query Match      10.7%  Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.043;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;

50 SSVYTSAMPGFPYPATAAAYR---GAHLRGGRVY-----YNTFRAAA 92
::: | | | | | | | | | | | | | | | | | | | | | | | |
2078 NNVIQLQPLPTPL-KITVIAVYEDGGHLTGNGRTYGLPPONIHISDEMYTRFRVSW 2136
DB

93 PPPPIAYGVVYQEPVYGNKLLQ---GGVAAARYAOPTPATAAAYSDSYGRVYAADPYH 149
| | | | | | | | | | | | | | | | | | | | | | | |
2137 DPSPVYGYKIYKVPVGSNPEMEAFVGEKTSYTL----- 2171
DB

150 HTLAPAPYGYGAMNAFA-----PLTDKTRSHADVGVLVSLQASIYQGYNRF 200
| | | | | | | | | | | | | | | | | | | | | | | |
2172 HNLNPSTTYDV---NVYAQYDSGLSVPLTDGTT-----LYLWVTDLKTYYQIGWDTF 2220
DB
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RESULT 6
US-10-177-293-63
Sequence 63, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumel
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Best Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puzsatic, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
```

```
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-63
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Query Match      10.7%  Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.043;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;

50 SSVYTSAMPGFPYPATAAAYR---GAHLRGGRVY-----YNTFRAAA 92
::: | | | | | | | | | | | | | | | | | | | | | | | |
2078 NNVIQLQPLPTPL-KITVIAVYEDGGHLTGNGRTYGLPPONIHISDEMYTRFRVSW 2136
DB

93 PPPPIAYGVVYQEPVYGNKLLQ---GGVAAARYAOPTPATAAAYSDSYGRVYAADPYH 149
| | | | | | | | | | | | | | | | | | | | | | | |
2137 DPSPVYGYKIYKVPVGSNPEMEAFVGEKTSYTL----- 2171
DB

150 HTLAPAPYGYGAMNAFA-----PLTDKTRSHADVGVLVSLQASIYQGYNRF 200
| | | | | | | | | | | | | | | | | | | | | | | |
2172 HNLNPSTTYDV---NVYAQYDSGLSVPLTDGTT-----LYLWVTDLKTYYQIGWDTF 2220
DB
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```
RESULT 7
US-10-012-952A-172
Sequence 172, Application US/10012952A
Publication No. US20030175707A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
TITLE OF INVENTION: Composition and Methods Relating to Prostate Specific Genes an
FILE REFERENCE: DEX-0263
CURRENT APPLICATION NUMBER: US/10/012,952A
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/246,039
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.1
SEQ ID NO 172
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-952A-172
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Query Match      8.8%  Score 96; DB 12; Length 388;
Best Local Similarity 24.9%; Pred. No. 0.3;
Matches 59; Conservative 16; Mismatches 86; Indels 76; Gaps 11;

21 GAVYSPDYACTVLLCONQSGSSMYSGPSSL-----VYTSAMGFYYPATATAAAYRG 74
| | | | | | | | | | | | | | | | | | | | | | | |
67 GGNFSVAAAANAANAANAQ-CRNLMAPAPLAPGASAYSSA-PGEAPPSAAAAA 124
DB

75 AHLRGRTVYNTFRFAAPPPPIAYGVVYQ-----EPVYGNKLLQGYAAYRY-- 124
QY
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8387
; LENGTH: 919
; TYPE: PRF
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8387

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Query Match      8.5%; Score 92.5; DB 15; Length 919;
Best Local Similarity 28.6%; Pred. No. 1.9;
Matches 36; Conservative 10; Mismatches 61; Indels 19; Gaps 5;

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QY 57 AMGFPYATAAAVGAHLRGRTYVTFRAAAPPEIPAVGVYQEPYGNKLLQ 116
DB 47 AYAGEAFEIGSGANALGGQLPAGGS--YGAY-----PPQQAAG--YQQPYGADPSQ 96
QY 117 GGAARVYAPPTATAAASDSYGRVYADPHHTLAPATYGVGAMNAPL----- 169
DB 97 MNAAAGYAPVTPPIAQMTOFGAMGVDP--HLMPPQQAQAAVAPQAPRVPYLNQLYP 154
QY 170 TDAKTR 175
DB 155 TDLTLQ 160

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RESULT 11
US-10-156-761-12012
; Sequence 12012, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: SHIBATA, YOSHIOKI
; APPLICANT: SAKAKI, YOSHIOKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12012
; LENGTH: 481
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12012

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Query Match      8.3%; Score 90.5; DB 15; Length 481;
Best Local Similarity 28.0%; Pred. No. 1.3;
Matches 47; Conservative 11; Mismatches 75; Indels 35; Gaps 7;

```

```

QY 26 PDFYAGTVLLCQANOGSSMSYSGPSS---LVYTS-AMGFPYATAAAVGAHLRGR 80
DB 298 PDSSSAVLIIRREGAGAGAGAGASESGRKTCLSQSSSECVETAPRGDAMGASVAAADLDGD 357
QY 81 GRTVYNTFRMAAPPPIPAVG-----GVVYQEPYGNKLLGGAAYRVAOPTPAT 131
DB 358 G-----AELVVGAPGEGVSLKSGSVTVLDGSEGPLSGSVT---YTQMPGI 404
QY 132 --AAAYSDSYGRVYADPHHTLAPATYGVGAMNAPL-----FAPLTD 171
DB 405 PGTAETADRFAGATLTAGPYHPGGRPLATGAPGENAKGCVWVPTTD 452

```

```

RESULT 12
US-10-156-761-11221
; Sequence 11221, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:

```

```

; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBATA, YOSHIOKI
; APPLICANT: SAKAKI, YOSHIOKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11221
; LENGTH: 342
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11221

```

```

Query Match      8.2%; Score 89.5; DB 15; Length 342;
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 52; Conservative 22; Mismatches 88; Indels 49; Gaps 11;

```

```

QY 6 AVNPYNGKLNLYV---GAVYSPDYAGTVLLCQANOGSSMSYSGPSSLYTSAMPGP 62
DB 56 ALDPRLVORVEAVETLGSAYGLDSAGYMANLEQRRGVRRGPPAHVY----- 106
QY 63 YPATAAAV---RGHLRGR-----GRVYNTFRMAAPPPIP-----AY 100
DB 107 -PYVPAACVFDLGRGDFRPRPAATGRAVEAAASEPAPVPEGCVAGTGAVYGQVK 165
QY 101 GGVYQEPYGNKLLGGAAYRVAOPT--PATAAAYSYSY-GR-VYADPHHTLAPAP 156
DB 166 GGVGTAFTVLSGSGITVAALVANAAGSTVDPETGVLYGELFGQGVVYPADGVHEA-ARRR 224
QY 157 TYVGAMNAPL-----TDAK--TRSHA 178
DB 225 LAETAAKNAPPPLNTTLAVVATDAELTKAQA 255

```

```

RESULT 13
US-10-156-761-10205
; Sequence 10205, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBATA, YOSHIOKI
; APPLICANT: SAKAKI, YOSHIOKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10205
; LENGTH: 363
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10205

```

```

Query Match      8.1%; Score 88.5; DB 15; Length 363;
Best Local Similarity 26.9%; Pred. No. 1.5;
Matches 50; Conservative 14; Mismatches 51; Indels 71; Gaps 12;

```

QY 65 AATAAAYRGAN-LRGR-----GRTVYNTFRA-----AAPP- 94
DB 191 AKTLEAVGRGQKHLGRISADDLGALTDGTPVGTSDADYLAGLADIGNPDPQSAPPQ 250
QY 95 -----PRPAAVGVYQEPYGNKLLGGYAAVRYAQPP-----ATAAAYSISYGRVAA 145
DB 251 TPQAPETPA-----QPOY-----GGQDAVAYXQOQTPDPYGYXQOYGQODAYGYOPTA 297
QY 146 DPYHHTLAPAPTYGVGANNAF-----APLT-DAKTRSH-ADDVGL---VLSSLOA 190
DB 298 DPY-----AAYPQOGIDQGTATDQNNQOGYSQPTQTHDSQPAQNDLDEASLFTSMISACQL 353
QY 191 SIYOGG 196
DB 354 RAYEOG 359

RESULT 14

S-10-156-761-11952

Sequence 11952, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11952
LENGTH: 380
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-11952

Query Match 8.1%; Score 88; DB 15; Length 380;

Best Local Similarity 25.1%; Pred. No. 1.8;

Matches 53; Conservative 15; Mismatches 61; Indels 82; Gaps 11;

DB 49 PSSLVYTSAMGPFY-----PAATA-----AAAYRGANLR-----GGRITY 85
DB 96 PSTVRYT-----GFPWHMIREELRLRPCTTLEVDLHADAEWHLRTGRLDAGRAALY 151
QY 86 NTFRAAAPPP-----IPAY-----GGVYOB-----P 108
DB 152 G---RVAPPPRRRTAYPAYKAVATILRSCHRRPEYGLHEDALGRVAHEGSHADIVLTP 208
QY 109 VYGNKLLGGYA---AYRYAQTPTATAAAYSISYGRVYAADPYHHTLAPAPTYG---VG 161
DB 209 FCGGAALPGFVPGPAPYPPEDQPRPTPDG-----PAAADVHNTIAAAVARGRHGEAD 260
QY 162 AMNAFAPLTDAKTRSHADVGLVLSLOAST 192
DB 261 ALAAQMEQTAASTHGAASEALHMRVRAIDL 291

RESULT 15

US-10-224-999A-3475

Sequence 3475, Application US/10224999A

Publication No. US20030171318A1

GENERAL INFORMATION:

APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott

APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3475
LENGTH: 2116
TYPE: PRT
ORGANISM: Rubella virus
US-10-224-999A-3475

Query Match 8.1%; Score 88; DB 12; Length 2116;

Best Local Similarity 31.7%; Pred. No. 15;

Matches 39; Conservative 8; Mismatches 50; Indels 26; Gaps 7;

QY 43 SSMYSGPSSLVYTSAMGPFYPPATATAAAYRGANLRGRTVYNTFRAAPP---PRIPA 99
DB 708 AAVRAGPQGSATSPPGDPPPRARRSQR--HIDAGTTPPAPARPPPPAPSPAPAP 765
QY 100 YGVVYQEPYGNKLLGGYAAVRYAQ-----TPPATAAAYSD---SYGRVYAAD 146
DB 766 RAG---DPVLYTS--AGPADRARHAELEVAVEPSDPTPTKADPDSDIVESYAR--AAG 817
QY 147 PYH 149
DB 818 PVH 820

Search completed: September 25, 2003, 12:07:56

Job time : 28 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 25, 2003, 11:56:35 ; Search time 53 Seconds
(without alignments)
1690.581 Million cell updates/sec

Title: US-09-809-545A-2
Perfect score: 1086
Sequence: 1 MTNKKAVNPYTNCKMLNPVY.....VLSSQASIVQGGYNRPAPY 203

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n.model -DEV=rlp
-Q/cgn2_1/USFTO.spool_E/US0980955/runat_25092003_111104_22915/app_query.fasta.1.391
-DB-issued.patents_NA -QFMT=fastap -SUFFIX=ini -MINMATCH=0 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bls0sum62 -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09809545 @CGN.1.1.85 @runat_25092003_111104_22915 -NCPu=6 -ICPu=3
-NO_MMAPP -LAREQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	955	87.9	2372	3	US-09-145-391-1
2	467.5	43.0	1506	3	US-09-176-657-5
3	467.5	43.0	1506	4	US-09-421-399-5
4	101	9.3	914	2	US-08-935-450-10
5	98.5	9.1	821	3	US-08-990-823-62
6	98.5	9.1	821	4	US-09-477-135A-62
7	97.5	9.0	4403765	3	US-09-103-840A-2
8	97.5	9.0	4411529	3	US-09-103-840A-1
9	96	8.8	3231	1	US-08-195-152-1
10	94.5	8.7	4403765	3	US-09-103-840A-2
11	94	8.7	2368	4	US-09-343-011B-3
12	94	8.7	43280	2	US-08-804-227C-1

13	92.5	8.5	2371	2	US-08-343-443B-1	Sequence 1, Appl1
14	92.5	8.5	2412	1	US-08-437-027-18	Sequence 1B, Appl
15	92.5	8.5	28958	1	US-08-258-261B-6	Sequence 6, Appl1
16	92.5	8.5	28958	1	US-08-456-837-6	Sequence 6, Appl1
17	92.5	8.5	28958	1	US-08-457-342-6	Sequence 6, Appl1
18	92.5	8.5	28958	1	US-08-457-646A-6	Sequence 6, Appl1
19	92.5	8.5	28958	1	US-08-458-076A-6	Sequence 6, Appl1
20	92.5	8.5	28958	1	US-08-764-233A-4	Sequence 4, Appl1
21	92.5	8.5	28958	1	US-08-457-235A-6	Sequence 6, Appl1
22	92.5	8.5	28958	1	US-08-729-214-6	Sequence 6, Appl1
23	92.5	8.5	28958	3	US-09-028-934-6	Sequence 6, Appl1
24	92.5	8.5	49377	1	US-08-764-233A-1	Sequence 1, Appl1
25	92.5	8.5	53526	3	US-08-658-136-2	Sequence 2, Appl1
26	92	8.5	53577	3	US-08-658-136-1	Sequence 1, Appl1
27	91	8.4	1896	4	US-09-343-011B-4	Sequence 4, Appl1
28	90.5	8.3	852	4	US-09-252-991A-16108	Sequence 16108, A
29	90.5	8.3	1311	4	US-09-252-991A-16493	Sequence 16493, A
30	90.5	8.3	10095	3	US-08-822-586-45	Sequence 45, Appl
31	90	8.3	2303	4	US-09-932-146-3	Sequence 3, Appl1
32	89.5	8.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
33	89	8.2	1083	4	US-09-252-991A-8817	Sequence 8817, Ap
34	89	8.2	1140	3	US-09-023-173-4	Sequence 4, Appl1
35	89	8.2	1227	4	US-09-252-991A-9232	Sequence 9232, Ap
36	89	8.2	1296	4	US-09-252-991A-9150	Sequence 9150, Ap
37	89	8.2	2715	4	US-09-252-991A-8715	Sequence 8715, Ap
38	88.5	8.1	2007	4	US-09-252-991A-3308	Sequence 3308, Ap
39	88.5	8.1	2709	4	US-09-252-991A-3326	Sequence 3326, Ap
40	88	8.1	885	4	US-09-252-991A-4426	Sequence 4426, Ap
41	88	8.1	1362	4	US-09-442-100-7	Sequence 4184, Ap
42	88	8.1	2923	6	US-09-252-991A-4104	Patent No. 5187076
43	87.5	8.1	3155	4	US-09-442-100-7	Sequence 7, Appl1
44	87.5	8.1	3155	4	US-08-939-106-7	Sequence 7, Appl1
45	87.5	8.1	44377	2	US-08-804-227C-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-145-391-1
Sequence 1, Application US/09145391
Patent No. 6194171
GENERAL INFORMATION:
APPLICANT: Pulist, Stefan M.
APPLICANT: Shibata, Hiroki
TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins.
TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/145.391
CURRENT FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (987)..(1979)
US-09-145-391-1

Alignment Scores:

Pred. No.: 2.56e-85
Score: 955.00
Percent Similarity: 86.94%
Best Local Similarity: 85.14%
Query Match: 87.94%
DB: 3
Caps: 2
US-09-809-545A-2 (1-203) x US-09-145-391-1 (1-2372)

QY 1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTrrPlyLsLeuAsnProValVal 20
Db 1572 ATGACAAATATAAAGACCGTCACCCCTTATACAAATGCTGGAATATGAAATTCACAGTTGTG 1631

```

QY      21  G1A1A1A1A1TyrSerProAspPheTyrAlaGlyThrValLeuLeuGlnAlaAsnGln 40
      1632  GGTGCAGTCTACAGTCCCAATTCATATGACGACAGGCTCTTGTGGCCAGCCAAACAG 1691
DB
QY      41  G1UG1YSerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
      1692  GAGGAGATCTTCATGATGACGATCCGCCACTTCATCTGTATATACCTTCAATTCGCCAGCC 1751
DB
QY      61  PheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
      1752  TTCCCGATCCAGACACCCACCCGCCGCCCTTACCGAGGCGCAGCTTGGCAGGCCCC 1811
DB
QY      81  G1A1A1A1A1TyrSerThrPheArgAlaAlaAlaProProProProLeuProAlaTyr 100
      1812  GGTCCACCGCTGACAAACCTTCAGGCGCGCGGCCGCCGCCGCCGATCCCGGCTAC 1871
DB
QY      101  G1G1G1A1A1ValTyr-GlnGluProValTyrGlyAsnGlyLeuLeuGlnGlyGlyAla 120
      1872  GCGGGTGTGTATACCCAGAGATGATTTATGTCGACAGC---ATTATATGCTGTTATGC 1928
DB
QY      120  A1A1A1A1A1TyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSer----- 138
      1929  TGCATATACCGCTACGCCACACCTTACCCCTTCCACTGCGCTGCTACAGTGACAG-AAATC 1987
DB
QY      139  -----TyrGlyArgVal 142
      1988  AGTTCGCTCTTCCTGACGACAGATGAATTTCTTGTAAACCTCTGACAGTTACGACAGACT 2047
DB
QY      142  1TyrAlaAlaAspProTyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAla 162
      2048  TTATGCTGCCAGCCCTTACACACGACTGCTGACGCCGCCACCTTACGCGGCTTGTGC 2107
DB
QY      162  A1A1A1A1A1PheAlaProLeuThrAspAlaTyrThrArgSerHisAlaAspAspValG1 182
      2108  CATGATGCTTTTGGACCTTGTACATGATGCCAAAGCTAGAGCCATGCTGATGATGTGG 2167
DB
QY      182  yLeuValLeuSerSerLeuGlnAlaSerTleTyrGlnGlyGlyTyrAsnArgPheAlaPro 202
      2168  TCTGCTCTTCTTCATATGACGCTAGTATATACGAGGGGATACACACGTTTGTCTCC 2227
DB
QY      202  OTTyr 203
      2228  ATAC 2231
DB

```

RESULT 2
US-09-176-657-5
Sequence 5, Application US/09176657
Patent No. 6020164

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Alina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/176, 657
CURRENT FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-09-176-657-5

Alignment Scores: 2,84e-37 Length: 1506
Pred. No.: 467.50 Matches: 107
Score:

Percent Similarity: 56.48% Conservative: 15
Best Local Similarity: 49.54% Mismatches: 39
Query Match: 43.05% Indels: 56
DB: 3 Gaps: 8

```

US-09-809-545a-2 (1-203) x US-09-176-657-5 (1-1506)
QY      1  MetThrAsnGlyLeuAlaValAsnProTyrThrAsnGlyTyrLysLeuAsnProValVal 20
      768  ATGACCAATTAACAGATGTTACACCATATTCGAATATGCTTGAATTAAGCCAGAGT 827
DB
QY      21  G1A1A1A1TyrSerProAspPheTyrAlaGlyThrValLeuLeuGlnAlaAsn--- 39
      828  GGAGCTGTATATGTCGCCGATATATGACGATTCAGGCTTCAAGACAGATGTGCCCTTA 887
DB
QY      40  ---GlnGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
      888  GGCATGATGACAGCAGTCCCTATCAGAGAGAGGGGATATACACTTACATTCCCTTTA 947
DB
QY      57  A1A1A1A1A1PheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
      948  ATCATTCCTGCTTCCCTTACCTTACCTACTGACGACGACGACGCGCTTTCAGAGAGCC 1007
DB
QY      76  HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
      1008  CATTTGAGGGGACAGAGGGGACAGATATATGCTGACATCCGA---GCGGTACTCCACAA 1064
DB
QY      96  ProLeuProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsnGlyLeu 115
      1065  GCCATCCCGCCCTATCC----- 1081
DB
QY      116  G1NG1G1G1TyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
      1082  ACGGGTGATATGACGCTTACAGATATGACAGCCGTGCTACTACGCAACCCACACCGCT 1141
DB
QY      132  -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
      1142  GCTGCAGCGCTGACAGCCCTTACAGGTGAGGTTATAGGAGGTTACACACCGACCC 1201
DB
QY      148  TyrHisHisThrLeuAlaProAlaProTyrTyrGlyValGlyAlaMetAsnAlaPheAla 167
      1202  TAC---CATGCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1246
DB
QY      168  ProLeuThrAspAlaTyrThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
      1246  ----- 1246
DB
QY      188  LeuGlnAlaSerTleTyrGlnGlyGlyTyrAsnArgPheAlaProTyr 203
      1247  -----GCGAGTTTATACCGAGGTGCTACACCGCATTTGCCCCCTTAC 1288
DB

```

RESULT 3
US-09-421-299-5
Sequence 5, Application US/09421299
Patent No. 6524579

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Alina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/421, 299
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: 09/176, 657
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA

```

; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-421-299-5

```

Alignment Scores:

Pred. No.:	2,846-37	Length:	1506
Score:	467.50	Matches:	107
Percent Similarity:	56.488	Conservative:	15
Best local Similarity:	49.548	Mismatches:	39
Query Match:	43.058	Indels:	56
DB:	4	Gaps:	8

US-09-809-545A-2 (1-203) x US-09-421-299-5 (1-1506)

Oy	1	MeThrHisnLysLysAlaValAsnProThrThrsnGlyTrpLysIleAsnProValAla	20
Db	768	ATGACCATTAGAAAGATGCTACACCATATCCAAATGGTGGAAATTAAAGCCAGTACT	827
Oy	21	GIAlaValAlaTrpSerProAspPheThrsValaGlyThrsValleuLeuCySGlnAlaAsn---	39
Db	828	GGAGCTGTATATGCGCGAGTATATATGACACATCCAGCTTTCAAGACGATGTGCTTA	887
Oy	40	---GlnGlnGlySerSerMetLysSerGlyProSerSerLeu-----ValTyrThrsSer	56
Db	888	GGCAATGATGACGAGAGTGCCCTTATCAGGAAGAGGGGTATCAACACTTACATTCCTTTA	947
Oy	57	AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaAlaTyrArgGlyAla	75
Db	948	ATCATTTCTGGCTTCCCTTACCTACATGTCAGACCACACGACGCCCTTTAGAGAGACC	1007
Oy	76	HisLeuArgGlyArgGlyArgThrsValTyrAsnThrPheArgAlaAlaAlaProProPro	95
Db	1008	CATTTTGAGGGGCAAGGGCGGACGATATGCTGACATGCCA---GGCGTACCTCCACAA	1064
Oy	96	ProIleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsnLysLeuLeu	115
Db	1065	GCCATTCGCCGCTATCC-----	1081
Oy	116	GlnGlnGlyTyrAlaAlaAlaTyrArgTyrAlaGlnProThrProAlaThr-----	131
Db	1082	AGGGGTGATATGACAGCTTACAGATATGACACAGCTGCTACTGCAACCGCAGCACCGCT	1141
Oy	132	-----AlaAlaAlaAlaTyrSerAspSerTyrGlyAlaGlyValTyrAlaAlaAspPro	147
Db	1142	GCTGCAGCCGCTGACGCGCTTACAGTACCGGTAATGGCAGGGGTCTACACGCGACGCC	1201
Oy	148	TyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla	167
Db	1202	TAC---CATGCCCTTGCCCGCTGCGGTACGTATGTGAGAGTTGGCGCTGTG-----	1246
Oy	168	ProLeuThrAspAlaLysThrArgSerHisAlaAspValGlyLeuValLeuSerSer	187
Db	1246	-----	1246
Oy	188	LeuGlnAlaSerIleTyrGlnGlyTyrAsnArgPheAlaProTyr	203
Db	1247	-----GGAGCTTTATACCGAGGTGGCTACAGCCGATTTGCCCTTAC	1288

```

RESULT 4
US-08-935-450-10
: Sequence 10, Application US/08935450
: Patent No. 5977311
:
: GENERAL INFORMATION:
:
: APPLICANT: Nandabalan, Krishnan
: APPLICANT: Yang, Meijia
: APPLICANT: Schulz, Vincent
: TITLE OF INVENTION: 53BP2 COMPLEXES
: FILE REFERENCE: 7954-054
: CURRENT APPLICATION NUMBER: US/08-935,450
: CURRENT FILING DATE: 1997-09-23
:
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatSeq Ver. 2.0

```

```
; SEQ ID NO 10
;;
;; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-935-450-10
```

Alignment Scores:

Pred. No.:	0.303	91
Score:	101.00	48
Percent Similarity:	37.06%	Conservative: 15
Best Local Similarity:	28.24%	Mismatches: 59
Query Match:	9.30%	Indels: 48
DB:	2	Gaps: 7

US-09-809-545A-2 (1-203) x US-08-935-450-10 (1-914),

Oy		2	TyrSerProAspheThryrLaclLynrhValleuSeuysgInalAasnIngLiUser	43
Db		230	TACAGCCCT-----GTCGGAAACCCCCCAGGGGCC	259
Oy		44	SerMetIyTserGIyProSerSerLeuValTyThrSeralA-MetProGIyPheProTy	63
Db		260	AGCACTACAATTAAGAAGAACCAACTCCCTGGCTCAACGCCCAATTACCAGCACCCCACC	319
Oy		63	rProAlaAlaThrala-----AlaAlaAlaTythrGrGLyAlahIsLieuArngLyAngGl	81
Db		320	GTCAGAGAGTACAGCCCTTCCACAGCCCGAGTTACAGCCACCCTTAC--AAACAGGG	376
Oy		81	yATrGrhVAlTyTrAsnThrPheArGrAlaAlaAlaA-ProProProPrOIleProAlaTyG	101
Db		377	GAGGTTCACAGCCAGGGGTTCACAGAGGCCACGCCCTCCACCTCCACACACACTGCCTCA	436
Oy		101	LylLylValValTyGrInglUproValTyGrILyAsnLyLyeuLeuIngLIgLyThyrrAla	121
Db		437	AC-----TATGGAGC-----TAGCGCGTTACACAC	463
Oy		121	LaTyArGrTyraLngrInProThrProAlaThrAlaAlaAlaTyTSerAspSerTyGrLyA	141
Db		464	CGGCCCCCATATACCCACCGCACCCACCCACCGCACAGACTTAC-----	507
Oy		141	rgvallyrrAlaAlaAspProTyGrHIShtshLyeuAlaProAlaProThrTyGrLyValG	161
Db		508	-----CTTCAGCCCACTATAACCACT	529
Oy		161	lYAlaMeTsnaIaPheaIaProLeuthrAspAlaLySThrArSerThIsLaAspaspy	181
Db		530	ATCAGACAGTATGCCACAGCTGAACACAGACTATATCAGAACAAGGGCCAGT-----	579
Oy		181	aIeGIyLeuValleuSerSerLeugIn	189
Db		580	--GGCGCCACTACTCGGAACCTACA	603

```

? RESULT 5
? US-08-990-823-62
? Sequence 62, Application US/08990823D
? Patent No. 6228371
? GENERAL INFORMATION:
? APPLICANT: Nano, Francis
? TITLE OF INVENTION: Mycobacterium tuberculosis DNA Sequences Encoding
? TITLE OF INVENTION: Immunostimulatory Peptides
? FILE REFERENCE: 49086
? CURRENT APPLICATION NUMBER: US/08-990,823D
? EARLIER APPLICATION NUMBER: US 96/10375
? EARLIER FILING DATE: 1996-06-14
? EARLIER APPLICATION NUMBER: 60/000,254
? EARLIER FILING DATE: 1995-06-15
? NUMBER OF SEQ. ID NOS: 113
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 62
? LENGTH: 821
? TYPE: DNA
? ORGANISM: Mycobacterium tuberculosis

```

FEATURE: ; NAME/KEY: Modified base ; OTHER INFORMATION: n represents a or g or c or t/u ; US-08-990-823-62

Alignment Scores: Pred. No.: 0.464 Length: 821 Score: 98.50 Matches: 59 Percent Similarity: 28.46% Conservative: 15 Best Local Similarity: 22.69% Mismatches: 95 Query Match: 9.07% Indels: 90 Gaps: 9

US-09-809-545a-2 (1-203) x US-08-990-823-62 (1-821)

```
Oy 1 MetThrAnLysLysAlaValAsnProTyrThrAsnGlyTyrPlysLeuAsnProValVal 20
Db 70 ATGCCCGACGACGCTCTGCGGAGCCGACCCCAATGCCGATGCTCAACCGGTTCCG 129
Oy 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAlaAsnGln 40
Db 130 GGCACGGCGTTCGACCGGACGAGCGCTGGGGGATCAGTCCGCTCGCTCAAAACCG 189
Oy 41 GluLysSerSerMetTyrSerGlyProSer-----SerLeuValTyr 54
Db 190 AGGCGGTGGCGGAGACCTCAAGTCCGACCCGGGTCTGCAACCCGGCGTGTCAAC 249
Oy 55 ThrSerAlaMetProGlyPheProTyrProAlaIleThrAlaIleAlaIleTyrArgGly 74
Db 250 TCCGATGCGTGGCCCAACAAACCCGACGACCGGCTCGCGGGGACCGCCGCGA 309
Oy 74 ----- 74
Db 310 GGAAGGCGCCGGNTCGGATNCAACGGGTTGCNACGGCGCTGCCCTGCGATTTGA 369
Oy 75 -----AlaHisLeuArgGlyArg-----GlyArgThrValTyr 85
Db 370 CCCGGCACGTACCCCGGTGATGGCGACGCTACGGGAGAACACCTGGCCGACCGCCAC 429
Oy 86 AsnThrPheArgAlaAlaIleAlaIleProProPheProIleProAlaIleTyrGlyValValTyr 105
Db 430 CTCGGCCGTGACCAAGTACCGCCCGGACCGCGCGCGGTGGT----- 480
Oy 106 GlnGluProValTyrGlyAsnLys-----LeuLeuGlnGlyGly----- 118
Db 481 -----GGTTTCCGGCGCGCGCATCTGCTCTCAAGGAGCGCGCATTTCACTGA 534
Oy 119 -----TyrAlaIleTyrArgTyrAlaGlnProThrProAlaThr 131
Db 535 CGGCCAGTCCCTGAACCTGACAGTGGGGCGCTACCGCGCGCGCATCTCAACCACT 594
Oy 132 AlaAlaIleTyrSerAspSerTyr----- 139
Db 595 GGGCAGGATATTTCGATCGACATCGACCGCAACCCGCGCCCATCTGCGGTTCC 654
Oy 140 -----GlyArgValTyrAlaIleAspProTyrHisHis----- 150
Db 655 GCTGGCCTGGCGCGCGCGGAGCGCGACGTGGCGG-----CATGTGTC 699
Oy 151 -----ThrLeuAlaIleProAlaIleProThrTyrGly 159
Db 700 CTATGACCCGAACTGAGCCCTGACCAATGGTTCGCTTCAGCCCGCCCGGTTCCGCT 759
Oy 160 ValGlyAlaMetAsnAlaPheAlaIleProLeuThrAspAlaIleGlnThrArgSerHisAlaAsp 179
Db 760 GCTGGAATCTCTGACGCGGTTGATCGGCTCAGCGACACCGGAGTGTGATGACATCGCAC 819
```

RESULT 6
US-09-477-135a-62
Sequence 62, Application US/09477135A
Patent No. 6572865
GENERAL INFORMATION:
APPLICANT: Nano, Francis

TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
FILE REFERENCE: 52888
CURRENT APPLICATION NUMBER: US/09/477, 135A
PRIOR APPLICATION NUMBER: 08890823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 62
LENGTH: 821
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(821)
OTHER INFORMATION: n = A, C, G, or T
US-09-477-135a-62

Alignment Scores: Pred. No.: 0.464 Length: 821 Score: 98.50 Matches: 59 Percent Similarity: 28.46% Conservative: 15 Best Local Similarity: 22.69% Mismatches: 95 Query Match: 9.07% Indels: 91 Gaps: 9

US-09-809-545a-2 (1-203) x US-09-477-135a-62 (1-821)

```
Oy 1 MetThrAnLysLysAlaValAsnProTyrThrAsnGlyTyrPlysLeuAsnProValVal 20
Db 70 ATGCCCGACGACGCTCTGCGGAGCCGACCCCAATGCCGATGCTCAACCGGTTCCG 129
Oy 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAlaAsnGln 40
Db 130 GGCACGGCGTTCGACCGGACGAGCGCTGGGGGATCAGTCCGCTCGCTCAAAACCG 189
Oy 41 GluLysSerSerMetTyrSerGlyProSer-----SerLeuValTyr 54
Db 190 AGGCGGTGGCGGAGACCTCAAGTCCGACCCGGGTCTGCAACCCGGCGTGTCAAC 249
Oy 55 ThrSerAlaMetProGlyPheProTyrProAlaIleThrAlaIleAlaIleTyrArgGly 74
Db 250 TCCGATGCGTGGCCCAACAAACCCGACGACCGGCTCGCGGGGACCGCCGCGA 309
Oy 106 GlnGluProValTyrGlyAsnLys-----LeuLeuGlnGlyGly----- 118
Db 481 -----GGTTTCCGGCGCGCGCATCTGCTCTCAAGGAGCGCGCATTTCACTGA 534
Oy 119 -----TyrAlaIleTyrArgTyrAlaGlnProThrProAlaThr 131
Db 535 CGGCCAGTCCCTGAACCTGACAGTGGGGCGCTACCGCGCGCGCATCTCAACCACT 594
Oy 132 AlaAlaIleTyrSerAspSerTyr----- 139
Db 595 GGGCAGGATATTTCGATCGACATCGACCGCAACCCGCGCCCATCTGCGGTTCC 654
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QY 140 -----GlyArgValTyrAlaAlaAspProTyrHisHis----- 150
DB 655 GGTGGCTGGGGCGCGCGAGAGCGACGTGGCGC-----CATGTGCG 699
QY 151 -----ThleuAlaProAlaProThrTyrGly 159
DB 700 CATGACCCGAACTGAGCCCTGAGCAATGTTGGCTTCACCCCGCGGTTCCGCT 759
QY 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAsp 179
DB 760 GCTGGAATCTCTGACAGCGTTGATCGGTCGACGACACCGCGTGTGATGACATCGCGAC 819

RESULT 7
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Alignment Scores:
Pred. No.: 6.01e+04 Length: 4403765
Score: 97.50 Matches: 66
Percent Similarity: 30.91% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 95
Query Match: 8.98% Indels: 96
Gaps: 12
DB: 3

US-09-809-545A-2 (1-203) x US-09-103-840A-2 (1-4403765)
1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTTrpLysLeuAsnProValVal 20
DB 4237678 ATGGCGGACGAGCTGTGGCCGACGCCCAATGCGCGCATGTGCAACCGGTTCCG 4237737
QY 21 GlyAlaValAlaTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyScInAlaAsnGln 40
DB 4237738 GGCACAGCGTTCGACGACGACGACGCGTGGGCGTATCAGTCCCTCGGCTTCAAAACC 4237797
QY 41 Glu-----GlySerSerMetTyrSerGlyPro-----SerSerLeuValTyr 54
DB 4237798 GAGGCGGTGGCGGACGACCTCAAGTCCGACCGGTGTCTCCAAACCGCGGTGTCAC 4237857
QY 55 ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaLysTyrArgGly 74
DB 4237858 TCCGATGCGTTCGCGCAACCAACCGACGCGCATACGACGACGCGCGGACCGCGGA 4237917
QY 75 AlaHisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaPro--- 93
DB 4237918 -----GGGAAGGCGCGGTGGGATCAACGGGTTCGACACGCGGTGCGCTTC 4237965
QY 94 -----ProProIleProAlaTyrGly----- 101
DB 4237966 GCATTGGACCGCGACGTCACCGGATGAGGGACGCTACGGGAGAACAACTGCGCGCC 4238025
QY 102 -----GlyValValTyrGlnGluPro----- 108

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DB 4238026 ACGGACCACTCGGCGCTGTACACAGTACCGCCCGGACCGGACCGCGCTGGTGGTG 4238085
QY 109 -----ValTyrGlyAsn 112
DB 4238086 GTTTCGCGCGCGCGCCATCTGTCCTACAGAGACGAGCGGATTCATCTACGCGCAG 4238145
QY 113 LysLeu---LeuGlnGlyGlyTyrAlaAlaLysTyrArgTyrAlaGlnProThrProAlaThr 131
DB 4238146 TCCCTGAACCTGCAGTG-GGG-----GTCACCGCGCGGACGCGCGCATCAGCACT 4238198
QY 132 AlaAlaAlaTyrSerAspSerTyr----- 139
DB 4238199 GGGGACGATATTCCGATGACATGACCGACCGAACCGCGGTGGCGCAATCTGCGGTTCC 4238258
QY 140 -----GlyArgValTyrAlaAlaAspProTyrHisHis----- 150
DB 4238259 GGTGGCTGGGGCGCGCGGACGACGCGACGCTGGCGC-----CATGTGCGC 4238303
QY 151 -----ThleuAlaProAlaProThrTyrGly 159
DB 4238304 CATGACCCGAACTGAGCCCTGAGCAATGTTCCGCTTCACCCCGCGGTTCCGCT 4238363
QY 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAsp 179
DB 4238364 GCTGGAATCTCTGACAGCGTTGATCGGTCGACGACGACGCGGTGATGACATCGCGAC 4238423
QY 180 AspValGlyLeuValIleuSerLeuGlnAlaSerIleTyrGln 194
DB 4238424 CGCAGCAACTT-----CCCTGCGCAGCGACCGTTCGCA 4238459

RESULT 8
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 6.02e+04 Length: 4411529
Score: 97.50 Matches: 66
Percent Similarity: 30.91% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 95
Query Match: 8.98% Indels: 96
Gaps: 12
DB: 3

US-09-809-545A-2 (1-203) x US-09-103-840A-1 (1-4411529)
1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTTrpLysLeuAsnProValVal 20
DB 4245432 ATGGCGGACGAGCTGTGGCCGACGCCCAATGCGCGCATGTGCAACCGGTTCCG 4245491
QY 21 GlyAlaValAlaTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyScInAlaAsnGln 40
DB 4245492 GGCACAGCGTTCGACGACGACGACGCGTGGGCGTATCAGTCCCTCGGCTTCAAAACC 4245551
QY 41 Glu-----GlySerSerMetTyrSerGlyPro-----SerSerLeuValTyr 54

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Db 4245552 GAGGCGCTGGCGGAGCACTCAAGTCCGAGCCGGTGTCTCCAAACCGCGGCTGTCAAC 4245611
Oy 55 ThrselametProglyPheProTyrProAlaIleThraIleAlaIleAlaIleTyrArgly 74
Db 4245612 TCCCATGCTGTCGCCCAACAAACCCACAGCCGCCATCACCGCATCCGGCGGACCGCGCGA 4245671
Oy 75 AlahIleuArglyArglyArglyThraValTyrAsnThrPheArgAlaIleAlaPro 93
Db 4245672 -----GGGAAGGCGCGGTGCGGATCAACGGGTGCGACAGCGGCGCTGCGCTC 4245719
Oy 94 -----ProProProIleProAlaTyrGly----- 101
Db 4245720 GGATTCGACCCGCACTACCCCGGTGTGTGGGAGCTACGGGAGAACACACCTGGCGCC 4245779
Oy 102 -----GlyAlaValTyrGlnIlePro----- 108
Db 4245780 ACGGCACTGCGGCTGTACACTTACCGCCCGGACCGCGGACCGCGCTGTGTG 4245839
Oy 109 -----ValTyrGlyAsn 112
Db 4245840 GTTTCGCGCGCGCGCCATCTGCTCTACAGAGAGAGCGCGGATTCATCTACGGCGAG 4245899
Oy 113 LysIleu---LeuGlnGlyGlyTyrAlaIleTyrArgTyrAlaGlnProThrProAlaThr 131
Db 4245900 TCCCTGAAACTGCACTG-666-----CGTCACGCGCGCGGAGCGCGCATCCAGCACT 4245952
Oy 132 AlahIleuArglySerAspSerTyr----- 139
Db 4245953 GGGCAGAGTATTTCCGATCGACATCGGACCGCAACCGCGCGGCAATCGCGGTTTC 4246012
Oy 140 -----GlyArgValTyrAlaIleAspProTyrHisHis----- 150
Db 4246013 GCTGGCTGGCGCGCGCGGAGCGCGACGTGGCGC-----CATGTGCG 4246057
Oy 151 -----ThrIleuAlaProAlaProThrTyrGly 159
Db 4246058 CTATGACCGCACTGAGCCTGAGCAATGTTGCTTCAACCCCGCGGTTCCGCT 4246117
Oy 160 ValGlyAlaMetAsnAlaPheAlaProIleuThrAspAlaIleTyrArgSerHisAlaAsp 179
Db 4246118 GCTGAATCTCTGAGCGGTTGATCGGTCAGCAGACCGGTTGATGACATCGCGAC 4246177
Oy 180 AspAlaGlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGln 194
Db 4246178 CGCAGCAACTT-----CCCTGTGCGAGCAGCGTTTCCGA 4246213

RESULT 9
-08-195-152-1
Sequence 1, Application US/08195152
Patent No. 5679541
GENERAL INFORMATION:
APPLICANT: Bonini, Nancy M.
APPLICANT: Leiserson, William M.
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,152
FILING DATE: 14-FEB-1994

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
US-08-195-152-1

Alignment Scores:
Pred. No.: 5.2 Length: 3231
Score: 96.00 Matches: 45
Percent Similarity: 37.57% Conservative: 23
Best Local Similarity: 24.86% Mismatches: 63
Query Match: 8.84% Indels: 51
DB: 1 Gaps: 6

US-09-809-545a-2 (1-203) x US-08-195-152-1 (1-3231)

Oy 42 GlySerSerMetTyr-----SerGlyProSerSerLeu 52
Db 1062 GGATCCAAATTGTATGCGGCTGCAGCTCGGCCGCAATCCGTGAGCGGAGGAGCGAGTGGG 1121
Oy 53 ValTyrThrSerAlaMetProGlyPheProTyrProAlaIleThrAlaIleAlaTyr 72
Db 1122 GTCAACTCTTTCGGAGTG-----GCAGGCGCAGCAGCGCGGTCTAC 1163
Oy 73 ArgGlyAlaHisIleuArglyArglyArglyThraValTyrAsnThrPheArgAlaIleAla 92
Db 1164 GACGGCAAACT-----GACTACTACTACTACACACACATGACAGATACAG 1211
Oy 93 ProProProIleProAlaTyrGlyValTyrGlnIleProValTyrGlyAsn 112
Db 1212 CCGCGCGCTCTCTCTCGGATACGGAATCTTATGGGCGGCGACGGCGGCGAG 1271
Oy 113 LysIleuLeuGlnGlyTyrAlaIleTyrArgTyrAlaGlnProThrProAlaThrAla 132
Db 1272 GCCAAGATGGAACCGGAGCGCGAGCTGGCGGCTGCTACTTACGCCCATGATGCC 1331
Oy 133 AlahIleu----- 134
Db 1332 GCCAGCGGCAACAACTCGCACTGACAGCTCCGTACGCCGCGCTACAACTTC 1391
Oy 135 -----TyrSerAspSerTyrGlyArgValTyrAlaIleAsp 146
Db 1392 GGGCAGCAGACTACGGGCGGCTACTACACAGACAGATGACGCACTATTACATGCGGCC 1451
Oy 147 ProTyrHisThrIleuAlaProIleuThrAspAlaIleTyrArgSerHisAlaAspVal 161
Db 1452 AACACTACACCGGTATGCGGTGACGCTCGCCAGCTGAGTGGAGTGCATGGCATGCTTC 1511
Oy 162 AlahIleuAlaPheAlaProIleuThrAspAlaIleTyrArgSerHisAlaAspVal 181
Db 1512 CATGTGGCGGCTCTGGAATCTCTCCGAGAGTCCACGAGACCCACTC-GACGAGGCC 1570
Oy 182 Gly 182
Db 1571 GGT 1573

RESULT 10
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.

```


; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 ; US-09-103-840A-2

Alignment Scores:

Pred. No.:	1.16e+05	Length:	4403765
Score:	94.50	Matches:	49
Percent Similarity:	42.26%	Conservative:	22
Best Local Similarity:	29.17%	Mismatches:	68
Query Match:	8.70%	Indels:	31
DB:	3	Gaps:	8

US-09-809-545a-2 (1-203) x US-09-103-840A-2 (1-4403765)

QY 11 ThrAsnGlyTrpLysLeuAsnProValAlaGlyValAlaValTyrSerProAspPheTyrAla 30
 Db 991136 ACAATGAGAGGCTGTGCAATCTCTACAGCGGGGGGGGGAGCT---GCTATACAG 991080
 QY 31 GlyThrValLeuLeuGlnAlaAsnGlnGluLysSerSerMetTyrSerGlyProSer 50
 Db 991079 GTGACCGAATGCTTTCGAGCGCGGAGAAAGATGCCGCGACCTGCGGACACCATTCG 991020
 QY 51 SerLeu-----ValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAla 68
 Db 991019 GCGACCGGCTGCTGTCTGACGCTGACAGCTTGTGGCTTACTTTGGCCAGATGTGGCTG 990960
 QY 69 Ala-----AlaAlaTyr-ArgGlyAlaHisLeuArgGlyArgGly----- 81
 Db 990959 GCATGTGACGAGGAGCCCTGAGCTATCCAGGAAATCAGCTGCCGAGGCGAGGACATCCA 990900
 QY 82 -----ArgThrValTyr-----AsnThrPheArgAlaAla 91
 Db 990899 ACGATGTGCGCAGAAAGGTTCTCGGCTATATACCAAGCCCAAGGTGC-TGGCGTATTGC 990841
 QY 91 AlaProProProProTyrProAlaTyrGlyValValTyrGlnGluProValTyrGly 111
 Db 990840 GCGGCG 990782
 QY 111 yAsnLysLeuLeuGlnGly---GlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAl 130
 Db 990781 CGGT---GTGTACCAAGGCAATGTGTATGCGGCGATACGATACGCC----- 990739
 QY 130 eThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspProTyrHisH 150
 Db 990738 ---GCGCTGCG 990683
 QY 150 sThrLeuAlaProAlaProThr 157
 Db 990682 ATTCTTAGGGCG 990661

RESULT 11
 ; US-09-343-011B-3
 ; Sequence 3, Application US/09343011B
 ; Patent No. 6300473
 ; GENERAL INFORMATION:
 ; APPLICANT: Stephanie Richard
 ; TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL

; TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
 ; FILE REFERENCE: A32561
 ; CURRENT APPLICATION NUMBER: US/09/343,011B
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: CA 2265271
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 2368
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-09-343-011B-3

Alignment Scores:

Pred. No.:	5.4	Length:	2368
Score:	94.00	Matches:	54
Percent Similarity:	36.93%	Conservative:	11
Best Local Similarity:	30.68%	Mismatches:	51
Query Match:	8.66%	Indels:	60
DB:	4	Gaps:	12

US-09-809-545a-2 (1-203) x US-09-343-011B-3 (1-2368)

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 Db 1733 CGTGGCGGTGCTGTGTCAC 1789
 QY 109 ValTyrLysLysLysLeuLeuGlnGly----- 117
 Db 1790 -----GGACCACTGTGACCCGCGGAGCTCTTCACGTGCCCAATAGCAGAGGTGC 1843
 QY 118 -----GlyTyrAlaAla-----TyrArgTyrAlaGlnProThr 128
 Db 1844 CCCACACCTGAGCGCGCGGAGCGGACGACGATACAGATACAGA---GCACCGCCACCT 1900
 QY 129 ProAlaThrAlaAla-----AlaTyrSerAspSerTyrGlyArgValTyrAla 144
 Db 1901 CCAGCTCATGATGCTTATGAAGAATATGATGATGATGATGATGATGATGATGATGATGAT 1960
 QY 145 AlaAspProTyr-----HisHisThrLeuAlaProAlaProThr 157
 Db 1961 GACCAGACCTATGAGCTTATGATATAGCTACGTGACCCACACACAAAGTGTGCTGAA 2020
 QY 158 -----TyrGlyValGly-----AlaMetAsnAlaPheAlaProLeuThr 170
 Db 2021 TACTATGACTACGTCTATGAGATGAACAGAGATGCCATGACAGCTACGACGAGAGAA 2080
 QY 171 AspAlaLysThrArgSerHisAlaAspValGlyLeuValLeuSerSerLeuGlnAla 190
 Db 2081 TGGGCCACACACTGCG-----TCACAGCTGAGAGCA 2110
 QY 191 -----SerLeuTyrGlnGlnGlyTyrAsnArgPheAlaProTyr 203
 Db 2111 CCACACCAAGGTGACGAGAGGGGATAC---AGGAGACACCCCTAT 2155

RESULT 12
 ; US-08-804-227C-1/C
 ; Sequence 1, Application US/08804227C
 ; Patent No. 5876991
 ; GENERAL INFORMATION:
 ; APPLICANT: DeHoff, Bradley S.
 ; APPLICANT: Kustoss, Stuart A.
 ; APPLICANT: Rostock, Paul R., Jr.
 ; APPLICANT: Sutton, Kimberly L.
 ; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: THOMAS G. PLANT 1501


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: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 2371 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
: FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 25..1992
:   US-08-343-443B-1
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: Alignment Scores:
: Pred. No.: 7.61 Length: 2371
: Score: 92.50 Matches: 48
: Percent Similarity: 33.72% Conservative: 10
: Best Local Similarity: 27.91% Mismatches: 73
: Query Match: 8.52% Indels: 41
: DB: 2 Gaps: 9
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: Db 109 TATGACAGACACC-----CAGCATATATGGGCAACAAAGCTATGGAACCTATGGA 159
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: Oy 48 GlyProSerSerLeuValYrThrThrSerAlaMetProGlyPheProTYrProAlaAlaThr 67
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: Oy 68 AlaAlaAlaIatYrIrglyAlaHisLeuArgGlyArgGlyAngThrValYrAsnThr 87
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:   ||||| :||| ||||| ||||| |||||
: Oy 128 ThrProAlaThrAlaAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 147
:   ||| :||| ||||| ||||| |||||
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: US-08-437-027-18
: Sequence 18, Application US/08437027
: Patent No. 5670317
: GENERAL INFORMATION:
:   APPLICANT: Landan1, Marc
:   APPLICANT: Gerald, William
:   TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
:   NUMBER OF SEQUENCES: 21
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Cooper & Dunham LLP
:   STREET: 1185 Avenue of the Americas
:   CITY: New York
:   STATE: New York
:   COUNTRY: U.S.A.

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1 ZIP: 0036
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Floppy disk
4 COMPUTER: IBM PC compatible
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6 SOFTWARE: Patentin Release #1.0, Version #1.30
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/08/437,027
9 FILING DATE:
10 CLASSIFICATION: 536
11 ATTORNEY/AGENT INFORMATION:
12 NAME: White, John P
13 REGISTRATION NUMBER: 28,678
14 REFERENCE/DOCKET NUMBER: 46416/JPM/CCA
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 212-278-0400
17 TELEFAX: 212-391-0525
18 INFORMATION FOR SEQ ID NO: 18:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 2412 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: cDNA to mRNA
25 US-08-437-027-18
26
27 Alignment Scores:
28 Pred. No.: 7.79 Length: 2412
29 Score: 92.50 Matches: 48
30 Percent Similarity: 33.72% Conservative: 10
31 Best Local Similarity: 27.91% Mismatches: 73
32 Query Match: 8.52% Indels: 41
33 DB: 1 Gaps: 9
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US-08-258-7618-6
Sequence 6, Application US/082582618
Patent No. 5639949
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Urnes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 25, 2003, 11:57:25 : Search time 169 Seconds
(without alignments)
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Title: US-09-809-545A-2
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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 1678620 segs, 1244745471 residues
Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	955	87.9	2372	9	US-09-794-591-1	Sequence 1, Appl1
3	500.5	46.1	1843	11	US-09-919-039-266	Sequence 266, App
4	467.5	43.0	1506	11	US-10-359-785-5	Sequence 5, Appl1
5	116	10.7	11447	12	US-10-301-822-25	Sequence 25, Appl
6	116	10.7	11447	14	US-10-177-293-60	Sequence 60, Appl
7	116	10.7	11560	14	US-10-177-293-62	Sequence 62, Appl
8	116	10.7	11657	14	US-10-198-846-11039	Sequence 11039, A
9	108.5	10.0	6930	13	US-10-098-841-226	Sequence 226, App
10	107	9.9	895	9	US-09-770-445-81	Sequence 481, App
11	102.5	9.4	1089	14	US-10-156-761-2655	Sequence 2655, App
12	102.5	9.4	9025608	14	US-10-156-761-1	Sequence 1, Appl1
13	99.5	9.2	5643	12	US-10-012-952A-43	Sequence 43, Appl
14	99	9.1	60	12	US-09-908-975-7420	Sequence 7420, App
15	99	9.1	864	13	US-10-027-632-18118	Sequence 18118, A
16	98.5	9.1	421	10	US-09-996-634-62	Sequence 62, Appl
17	98.5	9.1	821	11	US-09-997-182-62	Sequence 62, Appl
18	98.5	9.1	821	11	US-09-997-181-62	Sequence 62, Appl
19	97.5	9.0	2658	9	US-09-815-242-4035	Sequence 4035, App
20	97.5	9.0	3285	10	US-09-712-363-143	Sequence 143, App
21	96	8.8	3231	8	US-08-754-311B-1	Sequence 1, Appl1
22	95.5	8.8	9025608	14	US-10-156-761-1	Sequence 1, Appl1
23	94	8.7	657	10	US-09-974-300-1655	Sequence 1655, App
24	93	8.6	2076	14	US-10-156-761-7099	Sequence 7099, App
25	92.5	8.5	699	13	US-10-027-632-24830	Sequence 24830, A
26	92.5	8.5	699	13	US-10-027-632-24831	Sequence 24831, A
27	92.5	8.5	699	13	US-10-027-632-24832	Sequence 24832, A
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29	92.5	8.5	2390	10	US-09-880-107-3769	Sequence 3769, App
30	92.5	8.5	2390	12	US-09-873-319-717	Sequence 717, App
31	92.5	8.5	2390	12	US-09-960-706-1081	Sequence 1081, App
32	92.5	8.5	2760	14	US-10-128-714-7387	Sequence 7387, App
33	92.5	8.5	2902	14	US-10-128-714-6387	Sequence 6387, App
34	92.5	8.5	4514	14	US-10-128-714-387	Sequence 387, App
35	92.5	8.5	4902	14	US-10-128-714-5387	Sequence 5387, App
36	92	8.5	53522	11	US-09-904-968A-1	Sequence 1, Appl1
37	91.5	8.4	969	14	US-10-125-635A-452	Sequence 452, App
38	91	8.4	3673	14	US-10-157-031-332	Sequence 332, App
39	90.5	8.3	1443	14	US-10-156-761-4462	Sequence 4462, App
40	90.5	8.3	1743	10	US-09-887-576-788	Sequence 788, App
41	90.5	8.3	1869	14	US-10-156-761-3570	Sequence 3570, App
42	90.5	8.3	2804	12	US-10-023-782A-3	Sequence 3, Appl1
43	90.5	8.3	4340	14	US-10-198-846-12986	Sequence 12986, A
44	90	8.3	466	11	US-09-918-995-8298	Sequence 8298, App
45	90	8.3	1782	10	US-09-938-842A-1143	Sequence 1143, App

ALIGNMENTS

RESULT 1
US-09-809-545A-1
Sequence 1, Application US/09809545A1
Patent No. US20020110804A1
GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence W.
APPLICANT: White, R. Tyler
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS 017A
CURRENT APPLICATION NUMBER: US/09/809, 545A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1340
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-809-545A-1

Alignment Scores:

Pred. No.:	4.32e-117	Length:	1340
Score:	1086.00	Matches:	203
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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Db	595	GGCCGGGCTCTACAGCCCGGACTTCATTCAGGACGAGGTGCTGTGGCCAGGCCAAACAG	654	
Qy	41	GLuGlySerSerMetTyrSerGlyProSerSerLeuValLyrThrSerAlaMetProGly	60	
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Qy	61	PheProTyrProAlaAlaThrAlaAlaAlaAlaLyrArgGlyAlaHisLeuArgLysArg	80	
Db	715	TTTCGATATCCGGGGCCGACCTGCTGTACACTGCAATCCGAGGGGCTCACCTTGAGCGCT	774	
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Qy	101	GLyGlyValLyrLyrGlnGlyProValLyrGlyAsnLysLeuLysGlnGlyLysArg	120	
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Qy	161	GLyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysTyrArgSerHisAlaAspAsp	180	
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Qy	181	ValGlyLeuValLLeuSerSerLeuGlnAlaSerIleTyrGlnGlyLyrAsnArgPhe	200	
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: Patent No. US20010018198A1				
: GENERAL INFORMATION:				
: APPLICANT: Pulsat, Stefan M.				
: APPLICANT: Shibata, Hiroki				
: TITLE OF INVENTION: Nucleic Acids Related Atexin-2 Binding Proteins,				
: FILE REFERENCE: CE 3093				
: CURRENT APPLICATION NUMBER: US/09/794,591				
: PRIOR FILING DATE: 2001-02-26				
: PRIOR APPLICATION NUMBER: 09/145,391				
: NUMBER OF SEQ ID NOS: 2				
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: SEQ ID NO 1				
: LENGTH: 2372				
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: ORGANISM: Homo sapiens				
: FEATURE:				
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QY	61	PheProTYrProAlaAlaThrAlaAlaAlaAlaAlaTYrArgGlyAlaHisLeuArgGlyArg	80
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DB	1812	GGTGACACCGTGTACAAACACTTCAGGGCGCGGGGCCCGCCGATCCGGGCTAC	18711
QY	101	GLyGlyValValTYr-GlnGluProValTYrGlyAsnLysLeuLeuGlnGlyTYrAl	120
DB	1872	GGCGGTGTGTTATCCAGATGATTTATGATGTCAGAC--ATTATGCTGTTATGC	1928
QY	120	AlaLeTYrArGTYrAlaGlnProThrProAlaThrAlaAlaAlaTYrSerAspSer-----	138
DB	1929	TGCATACCGCTACGCCACGCTACCCCTGCCACATGCGCTGCTCAAGTGCAG-AAATC	1987
QY	139	-----TYrGlyArgVa	142
DB	1988	AGTTCGTTCTGTGCACAGATGAAATTTCTTGAACACCTCTGCAGTTACGAGCAGT	2047
QY	142	lTYrAlaAlaAspProTYrHisHisThrLeuAlaProAlaProThrTYrGlyValGlyAl	162
DB	2048	TTATGCTGCCACCCCTTACACACGACGACTGTCTCCACCCCCCCTACGCGCTTGTC	2107
QY	162	AlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAspAspValG	182
DB	2108	CATGATAGCTTTTGACACTTGTACTGATGACCAAGACTAGAGCCATGCTGATGATGCGG	2167
QY	182	ylLeuValLeuSerSerLeuGlnAlaSerIleTYrGlnGlyGlyTYrAsnArgPheAlaPr	202
DB	2168	TCTGTTCTTCTTCATATGCAGCGCATATATACGAGGGGAGATACAACGTTTTCGTC	2227
QY	202	CTyr	203
DB	2228	ATAC	2231

RESULT 3

US-09-919-039-266

; Sequence 266, Application US/09919039

; Publication No. US20030108871A1

; GENERAL INFORMATION:

; APPLICANT: Kaser, Matthew R.

; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

; FILE REFERENCE: PA-0035 US

; CURRENT APPLICATION NUMBER: US/09/919, 039

; CURRENT FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: 60/222, 113

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 401

; SOFTWARE: PERL Program

; SEQ ID NO 266

```

: LENGTH: 1843
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 1824
: OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

```

```

Alignment Scores:
Pred. No.: 1.32e-48 Length: 1843
Score: 500.50 Matches: 105
Percent Similarity: 52.61% Conservative: 6
Best Local Similarity: 49.76% Mismatches: 23
Query Match: 46.09% Indels: 77
DB: 11 Gaps: 5

```

US-09-809-545a-2 (1-203) x US-09-919-039-266 (1-1843)

```

QY 1 MethThrasnlyslsAlaValaAsnProTyrThrAsnGlyTrrplysleuAsnProVal 20
   |||||
Db 1228 ATGACCAACAAAGAGAGAGCGGGAACCCCTACACCAACGGCTGGAAGCTTAATCCAGTGTC 1287
QY 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValleuLeucysGlnAlaAsnGln 40
   |||||
Db 1288 GCGGCACTACAGCGGCTGAAATCTATGACAGTGACG----- 1323
QY 41 GluGlySerSerMetTyrSerGlyProSerSerleuValTyrThrSerAlaMetProGly 60
   |||||
Db 1324 -----GGG 1326
QY 61 PheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
   |||||
Db 1327 TTCCTCCATCCACACACCGGACACGCTGCTACCGGGGCGCACATCTTCGGGGCGCG 1386
QY 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProIleProAlaTyr 100
   |||||
Db 1387 GCGCGGGCGCTGTATATATACATTTCCGGCTGCGCCACCCCGCCCATCCGACTTAC 1446
QY 101 GlyGly----- 102
Db 1447 GGAGCGGACTGAGCAAAACGTTGTTAAATGCAAGTCCCATGGGCGGGGCTGGCACCG 1506
QY 102 ----- 102
Db 1507 TGGCCCTCCCTCCTCAGACAGACCGGAGCGGCTACCCACCTCTCCAGCGTTCCCA 1566
QY 103 -----ValValTyrGlnGluProValTyrGlyAsnLys 113
Db 1567 CCACCTTCTTGTCCGTTTGGCTTCCAGGGTGTGTATCAGATGATTTTAAATGCTGAG 1626
QY 114 LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAlaAla 133
   |||||
Db 1627 ---ATTATAGGAGCTACGACGCTACAGATACGCTCAGCCGCT---GGAAGGCGGCA 1680
QY 134 AlaTyrSerAspSerTyrGlyArgValTyr---AlaAlaAspProTyrHisHisThrLeu 152
   |||||
Db 1681 GCCTACAGCGACAGTTACGCGCAGAGTCTACGACAGCTGCCGACCCGTAACATCACACCATC 1740
QY 153 AlaProAlaProThrTyrGlyValGlyAlaMet 163
   |||||
Db 1741 GGGCGCGGCGGACCTACAGCATTTGCAACCATG 1773

```

```

RESULT 4
US-10-359-385-5
: Sequence 5, Application US/10359385
: Publication No. US20030143622A1
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom

```

```

: APPLICANT: Corley, Neil C.
: APPLICANT: Guejler, Karl J.
: APPLICANT: Lu, Aina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PE-0611 US
: CURRENT APPLICATION NUMBER: US/10/359,385
: CURRENT FILING DATE: 2003-02-05
: PRIOR APPLICATION NUMBER: US/09/176,657
: PRIOR FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: 1250374
US-10-359-385-5

```

```

Alignment Scores:
Pred. No.: 7.19e-45 Length: 1506
Score: 467.50 Matches: 107
Percent Similarity: 56.48% Conservative: 15
Best Local Similarity: 49.54% Mismatches: 39
Query Match: 43.05% Indels: 56
DB: 12 Gaps: 8

```

US-09-809-545a-2 (1-203) x US-10-359-385-5 (1-1506)

```

QY 1 MethThrasnlyslsAlaValaAsnProTyrThrAsnGlyTrrplysleuAsnProVal 20
   |||||
Db 768 ATGACCAATAGAAAGATGTCACACCATATGCAAAATGCTGGAATTAAGCCAGTAGTT 827
QY 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValleuLeucysGlnAlaAsn--- 39
   |||||
Db 828 GGAGCTGTATATGTCGCGAGTTATATGACATCCAGCTTTCACAGCATGTGTCCCTTA 887
QY 40 ---GluGlySerSerMetTyrSerGlyProSerSerleu-----ValTyrThrSer 56
   |||||
Db 888 GGCATATGTCACAGAGTCCCTATCAGAAAGGGGGGTATCAACATTACATTCCTTA 947
QY 57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
   |||||
Db 948 ATCATTCCTGCTGCTCCCTTACCTACTGACGACGACCGGCTTCAAGAGAGCC 1007
QY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
   |||||
Db 1008 CATTTAGGGGCGAGAGGGCGGACAGTATATGTGACAGTCCGA---GCGTACCTCCACA 1064
QY 96 ProIleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsnLysLeu 115
   |||||
Db 1065 GCCATCCCGCCATCC----- 1081
QY 116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
   |||||
Db 1082 AGGGGTGATATGACACCTATACATATGACACACCTGCTACCAACCGACGACCGCT 1141
QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
   |||||
Db 1142 GCTGACGCGCTCAGCCGCTTACGTACGAGTATATGGCGGCTGTACACAGCGGACCC 1201
QY 148 TyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
   |||||
Db 1202 TAC---CATGCCCTTCCCGCTGCGCTACGTATGAGAGTGGCGCTGG----- 1246
QY 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGlyLeuValleuSerSer 187
   |||||
Db 1246 ----- 1246
QY 188 LeuGlnAlaSerLeTyrGlnGlyGlyTyrAsnArgPheAlaProTyr 203
   |||||
Db 1247 -----GCGAGTTTATACGAGGTGCTACAGCGGATTTGCCCTTAC 1288

```

```

RESULT 5
US-10-301-822-25
; Sequence 25, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RMN
; CURRENT APPLICATION NUMBER: US/10/301.822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
US-10-301-822-25

Alignment Scores:
Pred. No.: 0.00979 Length: 11447
Score: 116.00 Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best Local Similarity: 25.14% Mismatches: 54
Query Match: 10.68% Indels: 64
DB: Gaps: 8

US-09-809-545A-2 (1-203) x US-10-301-822-25 (1-11447)
Y 50 SerSerLeuValITyThhSerAlaMetProGlyPheProTyPProAlaAlaThAlaLa 69
Db 6232 AACATGTAACACTGCACGCCCTGCACACCTGCACACTGCATCTATAT---AAATTAAGTATT 62888
Y 70 AlaAlaTyTArg-----GlyGlyAlaHisLeuArgGlyArgGlyArgThVal----- 84
Db 6289 GCTGTTTATGAAGATGCAGATGTGGCCATCTTAACAGGAATGGAGAACTGTGGACCTC 63488
Y 85 -----TyraenthPheArgAlaAlaLa 92
Db 6349 CTTCCTCCTCAGAACATACACATCTGTGACGAATGGTATACAAAGATTTCAGGCTGTCTCG 64088
Y 93 ProProProProlleProAlaTyGlyGlyAlaValTyGlnGluProValTyGlyAsn 112
Db 6409 GATCCTTCACCTCTCTCCAGTCTTGGAATATTAATAGATATTAAGCCAGTGGTTCCAAT 64688
Y 113 LysLeuLeuGln-----GlyGlyTyAlaAlaTyArgTyAlaGlnProThPro 129
Db 6469 GAGCCCATGGAGAGCCCTTTGTTGGAGAAATGACATCATATTAACCTTA----- 65133
Y 130 AlaThraAlaAlaAlaTySerAspSerTyGlyArgValTyAlaAlaAspProTyHis 149
Db 6513 ----- 65133
Y 150 HisThrLeuAlaProAlaProThTyTyGlyValGlyAlaMetAsnAlaPheAla----- 167

```

```

Db      6514 AACAAATCCAAATCCAGACACCAACCTACGATG-----AATGTTATGCAATAT 6564
Qy      168 -----ProLeuThraspAlaYThrArgSerHisAlaAspAla 181
Db      6565 GATTCCTGCAGCTACGTGTCCTTCGACATACAGGCATACA----- 6606
Qy      182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyTyrAsnArgPhe 200
      ||| |||::: ||||| |||::: |||
Db      6607 ---TTATATTTAATGTAACAGATCTGAAACTTACCAAGATTGGGTGGCATACATTC 6660

RESULT 6
US-10-177-293-60
; Sequence 60, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatc, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, ShubhangI
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongzao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzsai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
; FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-60

Alignment Scores:
Pred. No.: 0.00979 Length: 11447
Score: 116.00 Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best Local Similarity: 25.14% Mismatches: 54
Query Match: 10.68% Indels: 64
DB: 14 Gaps: 8

US-09-809-545A-2 (1-203) x US-10-177-293-60 (1-11447)
Qy      50 SerSerLeuValYrThrHisSerAlaMetProGlyPheProTyrProAlaThrAlaAla 69
      ::::::::::: ||| ||||| |||
Db      6232 AACATATGTAATCTGCAGCCCTCGCAACCTGACACTCATAT---AAAATTACTGTTATT 6288
Qy      70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgThrVal----- 84

```



```
Db 6289 GCTGTTATGAGATGAGATGATGCGCATCTACAGAAATGGAAGACTGTGGACTC 6348
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 85 -----TyrasnThrPheArgAlaAla 92
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6349 CTTCTCCTCGAGACATACACATCTGACGAATGATGATACAGATTCAGGTCCTGG 6408
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 93 ProProProIleProAlaTyrGlyValValTyrGlnGlnProValTyrGlyAsn 112
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6409 GATCCTCACCCTTCCTCCAGTTCTTGATATAAATAGATATTAAGCCAGTGGTCCAAAT 6468
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6469 GAGCCCATGGAAGCCTTGTGTGGAGAATGACATCATACCTTA----- 6513
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 130 AlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspProTyrHis 149
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6513 ----- 6513
Qy 150 HisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla----- 167
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6514 CACAAATCTCAATCCACACACACCTACGATGTG-----AATGTTATGCTCAATAT 6564
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 168 -----ProLeuThrAspAlaLysThrArgSerHisAlaAspVal 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6565 GATCTGACTGACTGTGCTCCCTGACAGATCAAGCAGCACTACA----- 6606
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPhe 200
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6607 ---TTAATATTAAATGTAAACAGATCTGAATACTTACAGATTTGGTGGATACATTC 6660
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 7

```
US-10-177-293-62
: Sequence 62, Application US/10177293
: Publication No. US20030124128A1
: GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Glatz, Karen
: APPLICANT: Zhao, Xumei
: APPLICANT: Gannavarpu, Manjula
: APPLICANT: Kamathkar, Shubhang
: APPLICANT: Mertens, Maureen
: APPLICANT: Myer, Vic
: APPLICANT: Wang, Youzhen
: APPLICANT: Xu, Yongyao
: APPLICANT: Hoersch, Sebastian
: APPLICANT: Monahan, John
: APPLICANT: Meyers, Rachel E.
: APPLICANT: Bast Jr., Robert C.
: APPLICANT: Hortobagyi, Gabriel N.
: APPLICANT: Puzstai, Lajos
: APPLICANT: Metic, Funda
: APPLICANT: Sahin, Aysegul
: APPLICANT: Mills, Gordon B.
: TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
: PREVENTION, AND THERAPY OF BREAST CANCER
: FILE REFERENCE: MRI-038
: CURRENT APPLICATION NUMBER: US/10/177,293
: CURRENT FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: US 60/299,887
: PRIOR FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: US 60/301,572
: PRIOR FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: US 60/306,501
: PRIOR FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: US 60/325,002
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US 60/362,585
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/xxx,xxx
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 506
: SOFTWARE: FastSeq for Windows Version 4.0
```

```
: SEQ ID NO 62
: LENGTH: 11560
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 10981
: OTHER INFORMATION: n = A,T,C or G
US-10-177-293-62
```

```
Alignment Scores:
Pred. No.: 0.0092 Length: 11560
Score: 116.00 Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best Local Similarity: 25.14% Mismatches: 54
Query Match: 10.68% Indels: 64
DB: 14 Gaps: 8
```

US-09-809-545a-2 (1-203) x US-10-177-293-62 (1-11560)

```
Qy 50 SerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAla 69
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6345 AACAAATGTAATGACGAGCCCTGCAACCTGACACTCCATAT---AAAATTACTGTTATT 6401
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgThrVal----- 84
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6402 GCTGTTATGAAATGAGATGAGATGTGGCCATCTACAGAAATGGAAGACTGTGGACTC 6461
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 85 -----TyrasnThrPheArgAlaAlaAla 92
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6462 CTTCTCCTCGAGACATACACATCTGACGAATGATATACAAAGATTCAGGTCCTGG 6521
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 93 ProProProIleProAlaTyrGlyValValTyrGlnGlnProValTyrGlyAsn 112
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6522 GATCCTCACCCTTCCTCCAGTTCTTGATATAAATAGATATTAAGCCAGTGGTCCAAAT 6581
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6582 GAGCCCATGGAAGCCTTGTGTGGAGAATGACATCATATACCTTA----- 6626
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 130 AlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspProTyrHis 149
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6626 ----- 6626
Qy 150 HisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla----- 167
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6627 CACAAATCTCAATCCACACACACCTACGATGTG-----AATGTTATGCTCAATAT 6677
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 168 -----ProLeuThrAspAlaLysThrArgSerHisAlaAspVal 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6678 GATCTGACTGACTGTGCTCCCTGACAGATCAAGCAGCACTACA----- 6719
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPhe 200
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6720 ---TTAATATTAAATGTAAACAGATCTGAATACTTACAGATTTGGTGGATACATTC 6773
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 8

```
US-10-198-846-11039
: Sequence 11039, Application US/10198846
: Publication No. US2003009974A1
: GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Xu, Yongyao
: APPLICANT: Wang, Youzhen
: APPLICANT: Steinmann, Kathleen
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: THERAPY OF BREAST CANCER
: FILE REFERENCE: MRI-049
: CURRENT APPLICATION NUMBER: US/10/198,846
: CURRENT FILING DATE: 2002-07-18
: PRIOR APPLICATION NUMBER: 60/306,220
: PRIOR FILING DATE: 2001-07-18
```

```

: NUMBER OF SEQ ID NOS: 14084
: SOFTWARE: fastseq for windows version 4.0
: SEQ ID NO 11039
: LENGTH: 11657
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1, 2, 3, 4, 11656, 11657
: OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11039

Alignment Scores:
Pred. No.: 0.01          Length: 11657
Score: 116.00           Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best Local Similarity: 25.14% Mismatches: 54
Query Match: 10.68%      Indels: 64
DB: 14                  Gaps: 8

-09-809-545A-2 (1-203) x US-10-198-846-11039 (1-11657)

QY 50 SerSerLeuValTyThrSerAlaMetProGlyPheProTyProAlaIaIaIa 69
DB 6398 AACATGTAATCTGACGCCCTGCACCTGCACCTCCATAT---AAATTTACTGTTATT 6454
QY 70 AlaAlaTyArg-----GlyAlaHisLeuArgGlyArgGlyArgVal----- 84
DB 6455 CCTGTTTATGAAGATGAGATGCGCCATCTAACAGAAATGGAAGAACTGGACATC 6514
QY 85 -----TyraStrThPheArgAlaIaIa 92
DB 6515 CTTCCTCTCAGACATACATCTCTGACGAATGATAAAGATTGCGGTGCTCTGG 6574
QY 93 ProProProIleProAlaTyArgGlyValValTyGlnIleProValTyArgGlyAsn 112
DB 6575 GATCCTTCACCTCTCCACCTCTTGTGATTAATAAGTATTAAGCCACCTGGTCCANT 6634
QY 113 LysLeuLeuGln-----GlyGlyTyAlaAlaTyArgTyArgIleProThrPro 129
DB 6635 GAGCCCATGGAAGCCTTGTGTGAGAAATGACATCATATACCTTA----- 6679
QY 130 AlaThrAlaAlaIaIaTySerAspSerTyArgIaValTyAlaAlaAspProTyHis 149
DB 6679 ----- 6679
QY 150 HisThrLeuAlaProAlaProThrTyArgIaValGlyAlaMetAsnAlaPheAla----- 167
DB 6680 CACATCTCAATCCACGACGACCTACGATG-----AATGTTTATCTCAATAT 6730
QY 168 -----ProLeuThrAspAlaLysThrArgSerHisAlaAspAspVal 181
DB 6731 GATTCTGACATCAGTGTCCCTTTCGACAGATCAAGGACACTACA----- 6772
QY 182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyArgGlnGlyGlyTyArgAsnArgPhe 200
DB 6773 ---TTATATTTAATGTAACAGATCGAAACTTACGAGATTGGGTGATACATTC 6826

RESULT 9
US-10-098-841-226
: Sequence 226, Application US/10098841
: Publication No. US20020197679A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Xu, Chongjun
: APPLICANT: Zhou, Ping
: APPLICANT: Ma, Yundong
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Zhao, Qian A.
: APPLICANT: Ren, Feiyun
: APPLICANT: Chen, Rui-hong

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: APPLICANT: Wang, Dunrui
: APPLICANT: Wang, Zhiwei
: APPLICANT: Wehrman, Tom
: APPLICANT: Zhang, Jie
: APPLICANT: Qian, Xiaohong B.
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
: FILE REFERENCE: 784CIP2
: CURRENT APPLICATION NUMBER: US/10/098,841
: PRIOR FILING DATE: 2002-03-13
: PRIOR APPLICATION NUMBER: 09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: 09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: 09/488,725
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 331
: SOFTWARE: PC_Fl_genes Version 1.0
: SEQ ID NO 226
: LENGTH: 6930
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (234) .. (968)
US-10-098-841-226

Alignment Scores:
Pred. No.: 0.0386       Length: 6930
Score: 108.50           Matches: 56
Percent Similarity: 35.85% Conservative: 20
Best Local Similarity: 26.42% Mismatches: 67
Query Match: 9.99%      Indels: 69
DB: 13                  Gaps: 12

US-09-809-545A-2 (1-203) x US-10-098-841-226 (1-6930)

QY 6 AlaValAsnProTyThrAsnGlyThrPylsLeuAsnProValValGlyAlaValTySer 25
DB 336 GCGTCAATCCC-----AGCTGTACCCGACCAATAGTCCAGTTATGCT 380
QY 26 ProAspPhe-----TyraIaGlyThrValLeuLeuGlyAlaAsn 39
DB 381 CCAGAGTTTCAGTCTCTGCGATTCAGCTTATGCA---ACTGCTGATGAAACAGGCCCTGG 437
QY 40 GlnGlnGlySerSer-----MetTySerGly 48
DB 438 CCACGAACTGCTCTTCTGTCGACCTGACGACCTTCACCTCCACGATGACGACCGG 497
QY 49 ProSerSerLeuValTyThrSerAlaMetProGlyPheProTyProAlaIaIaIa 68
DB 498 ACCGAGAACCGAATTTACCAAGCATCTCTGCGGCTTCAGATAT-----ACTGCG 548
QY 69 AlaAlaIaIaTyArgGlyAlaHisLeuArgGlyArgGlyArgValTyArgThrAsnThrPhe 88
DB 549 GGGACACCATACAG-----GTCCACACCGACCCAG 578
QY 89 ArgAlaAlaIaIaProProProIleProAlaTyArgIaValValTyArgGlnIlePro 108
DB 579 AGTACACTGCTCCACCCCTCTACTCCCATCACCAAC-----CCCTATCAGACGGCC 632
QY 109 ValTyR-----GlyAsnLysLeuGlnGlnGlyTyArgAla 120
DB 633 ATGTATCCAAATCAGAAAGTGCCTACCCGACGAGATCTGTATGCGGAGGAGCTTAC--- 689
QY 121 AlaTyArgTyArgIaGlnProThrProAlaThrAlaAlaIaIaTySerAspSerTyArgI 140
DB 690 -----TACACACACCG----- 701
QY 141 ArgValTyAlaAlaAspProTyR-----HisHisThrLeuAlaProAlaProThrTyR 158
DB 702 ---GTGTATGCTGCCAGCTTCATGTATCCACACACGACGAGGTCGTCACGCCAAC--- 755

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QY 159 GlyValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAla 178
Db 756 -----ACGATCCCTCTGCTGATGTACCCAGCACCTGTGGCCGCCGAGGACCAACGCT 809
QY 179 AspAspValGlyLeuValLeuSerSerLeuGlnAla 190
Db 810 GTGGCATGGGCGATGTGGCAGGACACCATGGCA 845

RESULT 10
US-09-770-445-481/c
; Sequence 481, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jom
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 202305 (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-481

Alignment Scores:
ed. No.: 0.00422 Length: 895
Score: 107.00 Matches: 52
Percent Similarity: 36.60% Conservative: 19
Best Local Similarity: 26.80% Mismatches: 63
Query Match: 9.85% Indels: 60
DB: 9 Gaps: 11

US-09-809-545A-2 (1-203) x US-09-770-445-481 (1-895)
QY 42 GlySerSerMetLysrSerGlyProSerSerLeuValLysrThrSerAlaMetProGlyPhe 61
Db 869 GGTCATGTGCTGTACCAAGTGTCA-----ACACCGAGCAGCAGCCGTATGTTAT 825
QY 62 ---ProLysrProAlaAla-----ThrAlaAlaAlaAlaLysrArgGlyAla 75
Db 824 GGTTCACACCGAGCAGCATGTGTATGTTCACTCCAGCAGCAGCATGTGTATGTTCA 765
QY 76 HisLeuArgGlyArg-----GlyArgThrValLysr 85
Db 764 AACGTGGCTCAGCAACAGCATATGTTATGCATCAAGTGGCTACGACAACTATAT 705
QY 86 AsnThrPheArgAlaAlaLysrPro-----ProProPhe 97
Db 704 CCTTCATATAGCTCTGTCAGCAGCAGCATGTGTATGTTATGTTATGTTATGTTATGTTAT 645

QY 98 ---ProAlaLysr-----GlyValValLysrGlnLysrPro 108
Db 644 GCCCGAGCTTATGAGCAGACAGCGGTCTCAGCCAGCTTGTGTGCAACAACTTCAGCT 585
QY 109 ValLysrGlyAsnLysrLeuGlnGlyValLysrAlaLysrArgLysrAlaGlnProThr 128
Db 584 GGGTACGGGCAAGTACCTCCAGACGGGTGCTATGTTGTTCCCTCCAGCAGACGGCT 525
QY 129 ProAlaThrAlaAlaLysrSerAsp---SerLysrGlyArgValLysrAlaLysrPro 147
Db 524 TATGTATATACCCCGCTCAAGCAGATGGAATCATGGA-----TCAATGCTCTCAG 471
QY 148 TyrHisHisThrLeuAlaProAlaProThrLysrGlyValGlyAlaMetAsnAlaPheAla 167
Db 470 TAT-----CTAGCTATGAGGTGGAAAGCATCAGATATGCT 432
QY 168 ProLeuThrAspAlaLysrThrArgSerHisAlaAspValGlyLeuValLeuSerSer 187
Db 431 GCACCTACTGGCCAAACCGCTATATCC----- 405
QY 188 LeuGlnAlaSerLysrLysrGlnGlyLysrLysrAlaArgPheAla 201
Db 404 ---CAGACTGCACCTCTCAGCGCGGTATGAGCAATCAGCA 366

RESULT 11
US-10-156-761-2655
; Sequence 2655, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHITUKU
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2655
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1089)
US-10-156-761-2655

Alignment Scores:
Pred. No.: 0.0181 Length: 1089
Score: 102.50 Matches: 48
Percent Similarity: 40.00% Conservative: 18
Best Local Similarity: 29.09% Mismatches: 55
Query Match: 9.44% Indels: 44
DB: 14 Gaps: 10

US-09-809-545A-2 (1-203) x US-10-156-761-2655 (1-1089)
QY 59 ProGlyPheProLysrProAlaAlaThrAlaAlaLysrArgGlyAlaLysrLeuArg 78
Db 636 CTTGGGGGCGCTCAGCAGCAGGAGGAGCGGCTCCAGCAGCAGCAGCGGCTACCT 695
QY 79 GlyArgGlyArgThrValLysrLysrPheArgAlaAlaLysrPro----- 94
Db 696 GCGCGGTCTGGCGGAGCAGTCCGAGCAACCGCCGAGCAGCGCTGCGCAGCGCGGAGCGCC 755

GenCore version 5.1.6
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Run on: September 25, 2003, 12:06:55; Search time 49 Seconds
(without alignments)
1333.157 Million cell updates/sec

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Perfect score: 796
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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4: /cgcn2_6/ptodata/1/lna/6B.COMB.seq:*
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6: /cgcn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	674	84.7	2372	3	US-09-145-391-1
2	379	47.6	1506	3	US-09-176-657-5
3	379	47.6	1506	4	US-09-421-299-5
4	93	11.7	914	2	US-08-935-450-10
5	92.5	11.6	28958	1	US-08-258-2618-6
6	92.5	11.6	28958	1	US-08-456-837-6
7	92.5	11.6	28958	1	US-08-457-342-6
8	92.5	11.6	28958	1	US-08-457-646A-6
9	92.5	11.6	28958	1	US-08-458-076A-6
10	92.5	11.6	28958	1	US-08-764-233A-4
11	92.5	11.6	28958	1	US-08-457-335A-6
12	92.5	11.6	28958	1	US-08-729-214-6

13	92.5	11.6	28958	3	US-09-028-934-6	Sequence 6, Appl1
14	92.5	11.6	49377	1	US-08-764-233A-1	Sequence 1, Appl1
15	91	11.4	821	3	US-08-990-823-62	Sequence 62, Appl1
16	91	11.4	821	4	US-09-477-135A-62	Sequence 62, Appl1
17	91	11.4	1896	4	US-09-343-011B-4	Sequence 4, Appl1
18	89.5	11.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
19	89.5	11.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
20	87.5	11.0	3231	1	US-08-195-152-1	Sequence 1, Appl1
21	86.5	10.9	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
22	86.5	10.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
23	85.5	10.7	1140	3	US-09-023-173-4	Sequence 4, Appl1
24	85.5	10.7	2208	4	US-09-620-312D-502	Sequence 502, App
25	85	10.7	53526	3	US-08-658-136-2	Sequence 2, Appl1
26	85	10.7	53577	3	US-08-658-136-1	Sequence 16, Appl1
27	84.5	10.6	1462	1	US-08-552-142A-16	Sequence 1, Appl1
28	84.5	10.6	1494	3	US-09-255-502-1	Sequence 1, Appl1
29	84.5	10.6	1496	6	RE34606-1	Patent No. RE34,60
30	84.5	10.6	1497	1	US-08-322-677A-6	Sequence 6, Appl1
31	84.5	10.6	1497	1	US-08-322-676-6	Sequence 6, Appl1
32	84.5	10.6	1497	3	US-08-898-218-6	Sequence 6, Appl1
33	84.5	10.6	1497	3	US-08-848-793-6	Sequence 6, Appl1
34	84.5	10.6	1497	4	US-09-445-270-1	Sequence 1, Appl1
35	84.5	10.6	1497	4	US-09-178-173A-1	Sequence 1, Appl1
36	84.5	10.6	1497	4	US-08-322-678-6	Sequence 6, Appl1
37	84.5	10.6	1497	6	5472855-1	Patent No. 5472855
38	84.5	10.6	1513	4	US-09-178-155-1	Sequence 1, Appl1
39	84.5	10.6	1868	1	US-08-069-863-1	Sequence 1, Appl1
40	84.5	10.6	1868	1	US-08-309-069-1	Sequence 1, Appl1
41	84.5	10.6	1868	1	US-08-562-833-1	Sequence 1, Appl1
42	84.5	10.6	1868	4	US-09-659-749-1	Sequence 1, Appl1
43	84.5	10.6	1868	4	US-09-672-105-1	Sequence 1, Appl1
44	84.5	10.6	1868	5	PCT-US95-05520-1	Sequence 1, Appl1
45	83.5	10.5	1352	1	US-08-552-142A-10	Sequence 10, Appl1

ALIGNMENTS

```
RESULT 1
US-09-145-391-1
; Sequence 1, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulist, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/145, 391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-145-391-1
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Alignment Scores:

Pred. No.:	4.26e-59	Length:	2372
Score:	674.00	Matches:	136
Percent Similarity:	83.23%	Conservative:	3
Best Local Similarity:	81.44%	Mismatches:	8
Query Match:	84.67%	Indels:	21
DB:	3	Gaps:	2

US-09-809-545A-2_COPY_1_148 (1-148) x US-09-145-391-1 (1-2372)

OY 1 MetTnAsnLysLysAlaValAsnProTyrTnAsnGlyTTrpLysLeuAsnProValVal 20
DB 1572 ATGACAAATATMAAAGACCTCAACCTTATACAAATGGCTGGAATTTGATCATCAGTTGTG 1631

OY 21 G1yAlaValTySerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsnGln 40
1632 GGTCAGCTATCAAGATCCCGAATTCTATGCAGGACGGTCCGTGTGCGACAGGCCAACAG 1691
OY 41 GluGlySerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
1692 GAGGGAATCTCCAGATCAGAGGCCCCAGTTCACTTATATACCTTCCTGCAGATCCAGGC 1751
OY 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
1752 TTCCCGATCCAGAGCCAGCCGCGCGCCCTACCGAGGGGGCCACCTGCGAGGCCGC 1811
OY 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProIleProAlaTyr 100
1812 GGTCGACCGGTACACACCTTCACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAC 1871
OY 101 G1yGlyValValTyr-GlnGluProValTyrGlyAlaAsnLeuGlnGlyTyrAl 120
1872 GCGCGTGTGTATACCGAGATGATGATTTATGTCAGAC---ATTATGTTGTTATGC 1928
OY 120 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSer----- 138
1929 TGCAATACCGCTACGCCAGCTACCTGCCACTGCGCTGCTACAGTGACAG-AAATC 1987
OY 139 -----TyrglyArgva 142
1988 AGTTCGTCTGTCGACAGATGAATTTCTGTACACCTCTGACAGTTACGAGCAGT 2047
OY 142 1TyrAlaAlaAspProTyr 148
2048 TTATGCTGCGACCCCTAC 2066
Db

RESULT 2

US-09-176-657-5
: Sequence 5, Application US/09176657
: Patent No. 6020164
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Alina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/09/176,657
: CURRENT FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
US-09-176-657-5

Alignment Scores:

Pred. No.: 1,92e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 3 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-176-657-5 (1-1506)

OY 1 MethThrsAnLysAlaValAsnProTyrThrAsnGlyTyrPlyLeuAsnProValVal 20
Db 768 ATGACCAATAGAAGATGTCACACACATATGCAAAATGTTGAATTAAGCCAGTATGTT 827
OY 21 G1yAlaValTySerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn--- 39

Db 828 GGAACCTATATGCTCCGAGATATATGACAGCATCCAGCTTTCAGCAGATGTGTCCCTA 887
OY 40 ---GlnGluGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
Db 888 GGCATATGACAGAGGCCCCCTATACAGAGAGGGGGGTATCAACTTACATTCCTTTA 947
OY 57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
Db 948 ATCATTCCTGCTCCCTTACCTTACCGACCCAGCCAGCCAGCGCGCTTTCAGAGAGGCC 1007
OY 76 HisLeuArgGlyArgGlyArgTyrValTyrAsnThrPheArgAlaAlaAlaProPro 95
Db 1008 CATTTGAGGGGACAGAGGCGGACATATATGTCAGTCCGA---GCGGTACCTCCACA 1064
OY 96 ProIleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAlaAsnLeu 115
Db 1065 GCCATCCCGCCCTATCC----- 1081
OY 116 GlnGlyAlaTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
Db 1082 AGGGGTGATATGACGCTACAGATATGACAGCGCTCTACTGCAACCGCAGCCAGCCGT 1141
OY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 1142 GCTGACCGCTGACGCGCTTACAGTACGAGCTTATGACAGGGTGTACACAGCCGACCC 1201
OY 148 Tyr 148
Db 1202 TAC 1204

RESULT 3

US-09-421-299-5
: Sequence 5, Application US/09421299
: Patent No. 6524579
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Alina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/09/421,299
: CURRENT FILING DATE: 1999-10-20
: EARLIER APPLICATION NUMBER: 09/176,657
: EARLIER FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
US-09-421-299-5

Alignment Scores:

Pred. No.: 1,92e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 4 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-421-299-5 (1-1506)

OY 1 MethThrsAnLysAlaValAsnProTyrThrAsnGlyTyrPlyLeuAsnProValVal 20
Db 768 ATGACCAATAGAAGATGTCACACACATATGCAAAATGTTGAATTAAGCCAGTATGTT 827
OY 21 G1yAlaValTySerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn--- 39

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Db 828 GGAGCTGTATATGTCGCGAGTATATGACAGATCCAGCTTTCAGCAGATGTGTCCCTA 887
Qy 40 ---GlnGlnGlnSerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
Db 888 GGCAATGATCAGCAGTACGCTTATCAGAGAGGGGGGTATCAACACTTACATTCCTTTA 947
Qy 57 AlameProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
Db 948 ATCATTCCTGCTTCCTTCCCTTACCTACTGACAGCCACCGCAGCTTTCAGAGGAGCC 1007
Qy 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
Db 1008 CATTTGAGGGGAGAGGGGCGGACAGTATATGTGCACTCGA---GGGTACCTCCACACA 1064
Qy 96 ProIleProAlaTyrGlyValValTyrGlnGlnProValTyrGlyAsnLysLeuLeu 115
Db 1065 GCCATCCCGCCCTATCC----- 1081
Qy 116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
Db 1082 AGGGGTGATATGACAGCTTACAGATATGACAGCTGCTCTGCAACCGCAGCCCGCT 1141
Qy 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 1142 GCTGACAGCCGCTGACAGCCGCTTACAGTACAGGTTATGACAGGGGTATGACAGCCGACCC 1201
Qy 148 Tyr 148
Db 1202 TAC 1204

RESULT 4
US-08-935-450-10
; Sequence 10, Application US/08935450
; Patent No. 5977311
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meljia
; APPLICANT: Schulz, Vincent
; TITLE OF INVENTION: 53BP2 COMPLEXES
; FILE REFERENCE: 7934-054
; CURRENT APPLICATION NUMBER: US/08/935,450
; CURRENT FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-935-450-10

Alignment Scores:
Pred. No.: 1 Length: 914
Score: 93.00 Matches: 39
Percent Similarity: 41.38% Conservative: 9
Best Local Similarity: 33.62% Mismatches: 42
Query Match: 11.68% Indels: 26
DB: 2 Gaps: 5

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-935-450-10 (1-914)

Qy 24 TyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyAlaAsnGlnGlnGlySer 43
Db 230 TACAGCCCT-----GCTGGAAACCCCGCCAGGGGCC 259
Qy 44 SerMetTyrSerGlyProSerSerLeuValTyrThrSerAla-MetProGlyPheProTyr 63
Db 260 AGCAGCTTACATAAGAACATCCCTGCTCAAGCCCAATACACACCCACCC 319
Qy 63 rProAlaAlaThrAla-----AlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 81
Db 320 GTCAGCAGCTACAGCCCTTCCACAGCCGAGTTACAGCCACCACTTAC--AAACGAGG 376

Qy 81 YArgThrValTyrAsnThrPheArgAlaAlaAla-ProProProIleProAlaTyrG 101
Db 377 GAGTTACAGCCAGGGTTACACAGCCCGCTCCACCTCCACACCACTGCTCCACA 436
Qy 101 lylGlyValValTyrGlnGlnProValTyrGlyAsnLysLeuLeuGlnGlyTyrAla 121
Db 437 AC-----TATGGAGC-----TACGGCGTTACANCC 463
Qy 121 lArTyrGlyTyrAlaGlnProThrProAlaThrAlaAlaTyr 135
Db 464 CGGCCCCCTATACCCACCGCCACCCCGCCACCGCACAGACTTAC 507

RESULT 5
US-08-258-261B-6
; Sequence 6, Application US/08258261B
; Patent No. 5639949
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James M.
; APPLICANT: Ligon, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,261B
; FILING DATE: 08-JUN-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-258-261B-6
Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

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US-09-809-545A-2_COPY_1_148 (1-148) x US-08-258-261B-6 (1-28958)
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Oy		47	SerGlyProSerGerdleUValTYTTrISerialMerPrGlyPheToTyLProAlala	66
Dd		10706	AGCGGGCCCTTCGCACATGGGCAATGCCGTCTCCTCGAGAAGTGACCSCCATCCCCGTCTCA	107655
OY		67	ThrAlalaaIlaaIatYT---ArgGLyaLnIs-LeuArGeLyarGLYaGrThrValty	85
Dd		10766	Ccctcccccscgcsgaacstggcgacgcsrtcacssgtctgaaccgccgttcgctgcagtgcatca	108225
OY		85	IasnthrrheaTGAALAAIALaRDrOrDrOrolLeProLAAtYGtLYaIVaITy	105
Dd		10826	TTCGAcS--AGAAAGAGCGCACCTGCGSSCSTGCTGTCTGCTGGGGGAgACTCTTA	108828
OY		105	rGlngILprovaLTyrOLysnlysuLeuInglnlgUTyUrTaIALaItYAgrTLl	125
Dd		10883	CCCAGGCSCT-----CGCGCTCGACTGGAAGACATTGTTCGCGCCCTTAGGCCCC	109333
OY		125	aGIn-----ProTHrPraLatHraAIaalatySeAsprserTy	139
Dd		10934	GCAAAGCTCTCCCTCCACCTACCCTCTCCAGCGAGAGCGGTTCTGCTCGAACGTCTCA	109939
OY		139	rGIytargVaITYrtaIAIaAsppro	147
Dd		10994	CGGACGAACGCTTCGACGTGCGCT	11018

RESULT 6
; Sequence 6, Application US/08456837
; Patent No. 5643774
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph

TITLE OF INVENTION: Genes for the syntheses of
NUMBER OF INVENTION: antipathogenic substances
CORRESPONDENCE ADDRESSES: 22
ADDRESSEE: Ciba-Gelgy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,837
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: type: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: US-08-456-837-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545A-2.COPY_1_148 (1-148) x US-08-456-837-6 (1-28958)
QY 47 SerGIyProSerSerLeuValTYrThrSerAlaMetProGlyPheProTYrProAlaAla 66
: ||||| |||::: ||| |||:::
Db 10706 AGGGGCTCTCGACATGGGCGATCGCTCTCCGCTCGAGGTCAAGCCCATCCCGTCTCA 107656
QY 67 ThAlAlAlAlAlAlAlATyr---ATggGlyAlaHis-LeuATggGlyATggGlyATgThValTY 85
: ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10766 CGCTCGCCCTCCCGCGAGACCTCGGAGCGCTCAGCCGCTGATCCCGTGTGCGGCTCCA 108235
QY 85 rAsnTYrPheATrAlAlAlAlAlAlAProProProProlleProAlATYrGlylValValTY 105
: ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10826 TTGAGAC---AGAAAGAAAGCGCACCTCGCCGCGCTGCTCTCTGCTGGGGGAGCTCTCTA 10882
QY 105 rGlnGluProValTYrGlylAsnLYsLeuLeuGlnGlyGlyTYrAlAlAlATyrATgTYrAl 125
: ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10883 CCGGAGGCT- - - - -CGCGCTCGACTGGAAAGACTTCTTGGCGCTCTAGCTCCCG 109333
QY 125 agIn- - - - -ProThrProAlAThrAlAlAlAlATyrSerAspSerTY 139
: ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10934 GCAGAGTCTCTCCCTCCACCTACCTCCCTTCACGAGAGCGGTTCTGCTCGACGTCTCCA 109939
QY 139 rGlyATrValTYrAlAlAlAlAlAlAspPro 147
: ||||| |||||
Db 10994 CGGACGAAACGCTTCGACGTGCGCT 11018

RESULT 7
US-08-457-342-6
: Sequence 6, Application US/08457342
: Patent No. 5662898
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Ligon, James M.
: APPLICANT: Beck, James Joseph
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Gaffney, Thomas Deane
: APPLICANT: Lam, Stephen Ting
: APPLICANT: Hammer, Phillip E.
: APPLICANT: Uknes, Scott Joseph
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0 Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/457,342
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/457,205
: FILING DATE: 01-JUN-1995
: APPLICATION NUMBER: 08/258,261
: FILING DATE: 08-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8614
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
:
: US-08-457-342-6
:
:
:
: Alignment Scores:
: Pred. No.: 106 Length: 28958
: Score: 92.50 Matches: 34
: Percent Similarity: 41.28% Conservative: 11
: Best Local Similarity: 31.19% Mismatches: 52
: Query Match: 11.62% Indels: 12
: DB: 1 Gaps: 4
:
: US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-342-6 (1-28958)
:
: QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10706 AGCGGCTCCCTCGAGAGGCGCATCGCTTCGCCGAGGAGCGAGCCCGCCGCTGCTCA 10765
:
: QY 67 ThrAlaAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgGlyArgGly 85
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10766 CGCTCGCCCTCGAGAGCGCTGCGAGCGCTGCGAGCGCTGCGAGCGCTGCGAGCGCTCA 10825
:
: QY 85 rAsnThrPheArgAlaAlaAlaAlaProProProProProProAlaTyrGlyGlyValValTyr 105
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10826 TTCGAGC--AGAGAGAGGCGCCACCTGCGCCGCTGCTTCCTCGGCGAGGCTCTCTA 10882
:
:   105 rGlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10883 CCGGAGGCGCT-----CGCGCTGCACTGGAAGGACTTCTCGGCCCTACCGCTCC 10933
:
: QY 125 agln-----ProThrProAlaThrAlaAlaAlaAlaTyrSerAspSerTyr 139
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10934 GCAAGGTCTCTCCCTCCACCTACCCCTTCACGAGAGCGGTTCTGCTGACGCTCTCA 10993
:
: QY 139 rGlyArgValTyrAlaAlaAlaAspPro 147
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10994 GCGAGCAAGCTTCCGACGCTGCTT 11018
:
: RESULT 8
: US-08-457-646a-6
: Sequence 6, Application US/08457646a
: Patent No. 5679560
:
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Ligon, James M.
: APPLICANT: Beck, James Joseph
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Gaffney, Thomas Deane
: APPLICANT: Lam, Stephen Ting

```

```

:
: APPLICANT: Hammer, Phillip E.
: APPLICANT: Uknes, Scott Joseph
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: City: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/457,646A
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/457,205
: FILING DATE: 01-JUN-1995
: APPLICATION NUMBER: 08/258,261
: FILING DATE: 08-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8614
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
:
: US-08-457-646a-6
:
:
:
: Alignment Scores:
: Pred. No.: 106 Length: 28958
: Score: 92.50 Matches: 34
: Percent Similarity: 41.28% Conservative: 11
: Best Local Similarity: 31.19% Mismatches: 52
: Query Match: 11.62% Indels: 12
: DB: 1 Gaps: 4
:
: US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-646a-6 (1-28958)
:
: QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10706 AGCGGCTCCCTCGAGAGGCGCATCGCTTCGCCGAGGAGCGAGCCCGCCGCTGCTCA 10765
:
: QY 67 ThrAlaAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgGlyArgGly 85
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10766 CGCTCGCCCTCGAGAGCGCTGCGAGCGCTGCGAGCGCTGCGAGCGCTGCGAGCGCTCA 10825
:
: QY 85 rAsnThrPheArgAlaAlaAlaAlaProProProProProProAlaTyrGlyGlyValValTyr 105
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10826 TTCGAGC--AGAGAGAGGCGCCACCTGCGCCGCTGCTTCCTCGGCGAGGCTCTCTA 10882
:
:   105 rGlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10883 CCGGAGGCGCT-----CGCGCTGCACTGGAAGGACTTCTCGGCCCTACCGCTCC 10933
:
: QY 125 agln-----ProThrProAlaThrAlaAlaAlaAlaTyrSerAspSerTyr 139
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10934 GCAAGGTCTCTCCCTCCACCTACCCCTTCACGAGAGCGGTTCTGCTGACGCTCTCA 10993

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IMMEDIATE SOURCE:
CLONE: p98/1
US-08-764-233A-4

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-764-233A-4 (1-23958)

QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
Db 10706 AGCGGCTCCTCGAGAGGCGCATCGCTTCGTCGAGGTACGCCCTCCACCTCCGTCTCA 10765

QY 67 ThrAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTy 85
Db 10766 CGCTCGGCTCCGCGAGACCTCGGAGGCGCTACCGCTCGATCCCGTGTGCTGCGCTCA 10825

QY 85 RasThrPheArgAlaAlaAlaProProProIleProAlaTyrGlyGlyValValTy 105
Db 10826 TTCGACG---AGAAAGAGGCCACCTCGCCGCTGCTCTCTCTGCGGCGAGCTCTCTA 10882

QY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
Db 10883 CCCGAGGCT-----CGCGCTCGACTGGAGAGACTTCTTGGCCCTACGCTCCCC 10933

QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
Db 10934 GCAAGTCTCCCTCCACCACTACCCCTTCCAGCGAGCGGTTCTGGCTGCAGCTCTCA 10993

QY 139 rGlyArgValTyrAlaAlaAspPro 147
Db 10994 CGGAGCAACGCTTCCGACGTGCCT 11018

RESULT 11
US-08-457-335A-6
Sequence 6, Application US/08457335A
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,335A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205

FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-457-335A-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-335A-6 (1-28958)

QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
Db 10706 AGCGGCTCCTCGAGAGGCGCATCGCTTCGTCGAGGTACGCCCACTCCGTCTCA 10765

QY 67 ThrAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTy 85
Db 10766 CGCTCGGCTCCGCGAGACCTCGGAGGCGCTACCGCTCGATCCCGTGTGCGCTCA 10825

QY 85 RasThrPheArgAlaAlaAlaProProProIleProAlaTyrGlyGlyValValTy 105
Db 10826 TTCGACG---AGAAAGAGGCCACCTCGCCGCTGCTCTCTCTGCGGCGAGCTCTCTA 10882

QY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
Db 10883 CCCGAGGCT-----CGCGCTCGACTGGAGAGACTTCTTGGCCCTACGCTCCCC 10933

QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
Db 10934 GCAAGTCTCCCTCCACCACTACCCCTTCCAGCGAGCGGTTCTGGCTGCAGCTCTCA 10993

QY 139 rGlyArgValTyrAlaAlaAspPro 147
Db 10994 CGGAGCAACGCTTCCGACGTGCCT 11018

RESULT 12
US-08-729-214-6
Sequence 6, Application US/08729214
Patent No. 5817502
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
CITY: Tarrytown

```

STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1506/CIPS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYDROLYTICAL: NO
ANTI-SENSE: NO

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Db      10934 GCAAGTCTCCTCCACCTACCCCTCCAGGAGCGCTTCGCTGACGCTCCCA 10993
QY      139 rGlyArgValTyrAlaAlaIAsPro 147
Db      10994 CGGAGCAACGCTTCGACGCTGCCT 11018

RESULT 14
US-08-764-233A-1
; Sequence 1, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes for The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Sorangium cellulosum
; IMMEDIATE SOURCE:
; CLONE: p98/1, pLJ3, and pVKM15
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 383..760
; OTHER INFORMATION: /product= "Sora"
; OTHER INFORMATION: /note= "This gene encodes a protein that is highly homologous
; OTHER INFORMATION: the reductase domains of type I PKSs such as eryA from
; OTHER INFORMATION: Saccharopolyspora erythraea."
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 927..19874
; OTHER INFORMATION: /product= "Sora"
; OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKSs that
; OTHER INFORMATION: are known to be involved in the synthesis of polyketide
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; OTHER INFORMATION: compounds."
; FEATURE:
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; LOCATION: 942..7115
; OTHER INFORMATION: /product= "Module 1 of Sora"
; FEATURE:
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; LOCATION: 7203..12884
; OTHER INFORMATION: /product= "Module 2 of Sora"
; FEATURE:
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; LOCATION: 13455..19616
; OTHER INFORMATION: /product= "Module 3 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 19870..24556
; OTHER INFORMATION: /product= "Module 1 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 24638..30820
; OTHER INFORMATION: /product= "Module 2 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 30881..35446
; OTHER INFORMATION: /product= "Module 3 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 35528..40114
; OTHER INFORMATION: /product= "Module 4 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 40190..46318
; OTHER INFORMATION: /product= "Module 5 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 46851..47891
; OTHER INFORMATION: /product= "Sora"
; OTHER INFORMATION: /note= "The protein encoded by the sora gene is highly
; OTHER INFORMATION: homologous to the methyltransferase from Streptomyces
; OTHER INFORMATION: hygroscopicus that is involved in the synthesis of the
; OTHER INFORMATION: polyketide rapamycin."
; US-08-764-233A-1

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Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

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QY 67 ThrAlaAlaAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 85
Db 27069 CGCTCCGCTCCGACGACCTGCGACGCTGCGATCCGCTGCTGCTGCTGCTGCTCA 27128
QY 85 rAsnThrPheArgAlaAlaAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 105
Db 27129 TTCGAGC---AGAGAAGGCGACCTGCGCGCTGCTGCTGCTGCTGCTGCTCA 27185
QY 105 rGlnGluProValTyrGlyAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 125
Db 27186 CCGGAGGCGCT-----CGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27236
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QY 125 acIn-----ProThrProAlaThrAlaAlaTyrSerAspSerTy 139
DB 27237 GCAAGCTCTCCCTCCCACTACCCCTTCACGAGAGCGGTTGCGTCGACGCTCTCA 27296
QY 139 rGlyArgValTyrAlaAlaAspPro 147
DB 27297 CGGACGAACGCTTCCGACGTCGCT 27321

RESULT 15
US-08-990-823-62
; Sequence 62, Application US/08990823D
; Patent No. 6228371
; GENERAL INFORMATION:
; APPLICANT: Nano, Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; TITLE OF INVENTION: Immunostimulatory Peptides
; FILE REFERENCE: 49086
; CURRENT APPLICATION NUMBER: US/08/990,823D
; CURRENT FILING DATE: 1997-12-15
; EARLIER APPLICATION NUMBER: US 96/10375
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: 60/000,254
; EARLIER FILING DATE: 1995-06-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: Modified base
; OTHER INFORMATION: n represents a or g or c or t/u
US-08-990-823-62

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Score: 91.00 Matches: 45
Percent Similarity: 30.85% Conservative: 13
Best Local Similarity: 23.94% Mismatches: 76
Query Match: 11.43% Indels: 54
DB: 3 Gaps: 6

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QY 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAlaAsnGln 40
DB 130 GGCCAGCGCTTCGACGCGACGCGATGCGGCGTATCATGCCGCTGCAAAACCG 189
QY 41 GluLysSerSerMetTyrSerGlyProSer-----SerLeuValTyr 54
DB 190 AGGCGCTGGCGAGGAGCTCAAGTCCGANCCCGGTGCTCCAAACCGGCGGTGTCAC 249
QY 55 ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrArgGly 74
DB 250 TCCGATGCGTGGCCCAACAAACCGCGCATCAGACTCCGCGGCGACCGCGCA 309
QY 74 ----- 74
DB 310 GGGAAGGCGCGGNTCGGATNCAAGGGTTGCNAGCGCGCTGCCGTCNGATTTGA 369
QY 75 -----AlaHisLeuArgGlyArg-----GlyArgThrValTyr 85
DB 370 CCCGCGACGTACCCCGCGGATGGGAGGAGAACAACTGCGCGCGCACGCGCAC 429
QY 86 AsnThrPheArgAlaAlaAlaProProProProAlaTyrGlyGlyValValTyr 105
DB 430 CTCGGCCGTGTACCAAGTACCGCCCGCGACCGCGCGCGGTGTGT----- 480

QY 106 GlnGluProValTyrGlyAsnLys-----LeuLeuGlnGly----- 118
DB 481 -----GGTTTCGCGCGCGCGCCCATCTGTGTCTACAAGAGAGACGCGGATTCATCTA 534
QY 119 -----TyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
DB 535 CGGCGAGTCCCTGAACACTGCAAGTGGGCGGTCCACGCGCGGACGCGCGCATCAGCCACT 594
QY 132 AlaAlaAlaTyrSerAspSerTyr 139
DB 595 GGGCAGGATTTCCGATCGACAT 618

Search completed: September 25, 2003, 12:13:58
Job time: 102 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 25, 2003, 12:07:20; Search time 148 Seconds
(without alignments)
2489.491 Million cell updates/sec

Title: US-09-809-545A-2_COPY_1_148
Perfect score: 796
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1678620 seqs, 1244745471 residues
Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USRR=US09809545 @cgn_1.1.85 @runatc_25092003_111136_23219
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-LONGLOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	441.5	55.5	1843	11	US-09-919-039-266
4	379	47.6	1506	12	US-10-359-385-5
5	94	11.8	657	10	US-09-974-300-1655
6	92.5	11.6	699	13	US-10-027-632-24830
7	92.5	11.6	699	13	US-10-027-632-24831
8	92.5	11.6	699	13	US-10-027-632-24832
9	92.5	11.6	11447	12	US-10-027-632-24832
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12	92.5	11.6	11447	12	US-10-027-632-24832
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14	91	11.4	821	11	US-09-997-182-62
15	91	11.4	821	11	US-09-997-182-62
16	90	11.3	466	11	US-09-918-995-8998
17	89.5	11.2	3285	10	US-09-712-363-143
18	89	11.2	1089	14	US-10-156-761-2655
19	87.5	11.0	2658	9	US-09-815-242-4035
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21	87.5	11.0	3231	8	US-08-754-311B-1
22	87.5	11.0	4182	12	US-09-814-353-20319
23	87.5	11.0	10278	12	US-09-820-788-3
24	86	10.8	1963	12	US-10-205-219-182
25	86	10.8	2179	13	US-10-027-632-97742
26	85.5	10.7	2208	14	US-10-037-270-502
27	85	10.7	1383	14	US-10-156-761-3834
28	85	10.7	1743	10	US-09-887-576-788
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31	85	10.7	9025608	14	US-10-156-761-1
32	84.5	10.6	969	14	US-10-125-653A-452
33	84.5	10.6	1494	14	US-10-104-693-1
34	84.5	10.6	1497	9	US-08-322-678-6
35	84.5	10.6	1497	9	US-09-060-854B-1
36	84.5	10.6	1497	14	US-10-033-325-1
37	84.5	10.6	1497	14	US-10-228-572-1
38	84.5	10.6	4244	11	US-09-760-285-27
39	84.5	10.6	4244	12	US-10-240-965-250
40	84.5	10.6	4264	11	US-09-912-697-15
41	84.5	10.6	4264	12	US-10-270-839-36
42	84.5	10.6	4264	12	US-10-371-634-16
43	84.5	10.6	4264	12	US-10-348-074-41
44	84.5	10.6	4264	14	US-10-171-581-28
45	84.5	10.6	62944	10	US-09-954-456-2257

ALIGNMENTS

RESULT 1
US-09-809-545A-1
; Sequence 1, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS 017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-809-545A-1

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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Sequence 266, App
Sequence 5, Appl1
Sequence 1655, Ap
Sequence 24830, A
Sequence 24831, A
Sequence 24832, A
Sequence 25, Appl
Sequence 60, Appl
Sequence 62, Appl
Sequence 11039, A
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 143, App
Sequence 2655, Ap
Sequence 1, Appl1
Sequence 4035, Ap
Sequence 20319, A
Sequence 3, Appl1
Sequence 182, App
Sequence 97742, A
Sequence 502, App
Sequence 3834, Ap
Sequence 788, App
Sequence 226, App
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 452, App
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Sequence 15, Appl1
Sequence 36, Appl1
Sequence 16, Appl1
Sequence 41, Appl1
Sequence 28, Appl1
Sequence 2257, Ap

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Db      1632  GGTCAGACGTCACATCCCGCATTCATGACGACGCGTCCGTGTGTCCAGGCGCACAG 1691
Qy      41    GluGlySerSerMetTySerGlyProSerSerLeuValTyrrHrSerAlaMetProGly 60
Db      1692  GAGGAGATCTTCATGTACAGTACAGTCCCGCAGTGCATCTTATATACCTTGTGCAGATGCCAGGC 1751
Qy      61    PheProTyrrProAlaAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
Db      1752  TTCCCGATTCACAGACGACCGCCGCCGCCGCCCTACCGAGGGGGCGACACTGCCAGGCGCC 1811
Qy      81    G1yArGtHrVal1yTyraSnThrPheArGAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 100
Db      1812  GGTCGACACCGGTGTCAACACCTTCAGGCGCCGCCGCCGCCCGCCCGCATCCCGGCTTAC 1871
Qy      101  G1yG1yAlaVal1yTyrr-GlnGluProVal1yTyG1yAsnH1yS1euleuGlnG1yTyra1 120
Db      1872  GCGCGGTGTGTTCACCGAGATGATTTATAGTGCAGAC-...ATTATGGTGGTATATGC 1928
Qy      120  aAlaTyrrArGtTyraGlnProThrProAlaThrAlaAlaAlaAlaAlaTyrrSerAspSer----- 138
Db      1929  TGCATACCGCTACCGCCAGCCTTACCCTGCCACATGCCGTGCCCTACAGTGCAG-AAATC 1987
Qy      139  -----TyrrG1yArGva 142
Db      1988  AGTTCGTCCTTCGTTGCAGCAGATGAATTTCTTGTACACCTCTGCAGTTACGAGCAGT 2047
Qy      142  1TyrrAlaAlaAspProTyrr 148
Db      2048  TTATGCTGCAGACCCCTTAC 2066

RESULT 3
US-09-919-039-266
; Sequence 266: Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 266
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
; NAME/KEY: unsure
; LOCATION: 1824
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

Alignment Scores:
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Score:          441.50      Matches:      96
Percent Similarity: 51.02%      Conservative: 4
Best Local Similarity: 48.98%      Mismatches:  19
Query Match:     55.46%      Indels:      77
DB:              11          Gaps:        5

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      1288 GGGCGAGTCTACGCGGCTGATTCATTCAGTACG----- 1323
QY      41  GlnGlySerSerMetYrSerGlyProSerSerLeuValYrThrSerAlaMetProGly 60
      1324 -----GGG 1326
QY      61  PheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
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QY      81  GYArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProleuProAlaTyr 100
      1387 GGGCGGCGCGTGTATATATTCATTTGGGGTGGCCACCCACCCCGCATCCGACTTAC 1446
QY      101  GlyGly----- 102
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QY      102 ----- 102
Db      1507 TGGCCCTCCCTCCCTCAGCAGACCGGCGCCCTACCCCACTCTCCAGCGTTCCCA 1566
QY      103 -----ValValTyrGlnGluProValTyrGlyAsnLys 113
      1567 CCACCTTCCTGTCGCTTGTGCTTCCAGGTCGTGTATCAGAGATGGANTTTATGTGTGAG 1626
QY      114  LeuLeuGlnGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAlaAla 133
      1627 ---ATTATGAGAGGTACGACGAGCTACAGATACGTCAGGCCCT---GGAGCGGGGCA 1680
QY      134  AlaTyrSerAspSerTyrGlyArgValTyr---AlaAlaAspProTyr 148
      1681 GCCTACAGCGACAGTTACGCGACAGTCTACGAGCTGCGACCCGCTAC 1728

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RESULT 4

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US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-5

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Alignment Scores:

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Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 12 Gaps: 6

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QY      21  GYAlaValTyrSerProAspPheYrAlaGlyThrValLeuLeucysGlnAlaAsn--- 39
      828 GGAGCTGTATATGCTCCGAGATTATGCAGCATCCAGCTTTCACACAGATGTGTCCCA 887
QY      40  ---GlnGlySerSerMetYrSerGlyProSerSerLeu-----ValYrThrSer 56
      888 GGCAATGATGACAGACTGCCCTATCAGGAAGAGGGGTATCAACACTTACATTCCTTAA 947
QY      57  AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
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QY      76  HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProproPro 95
      1008 CATTGAGGGGCGACAGAGGGCGGACAGATATGTGTGAGTCCGA---CGGTTACTCCACA 1064
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      1065 GCCATCCCGCGCTATCC----- 1081
QY      116  GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
      1082 AGGGGTGATATGACACCTTACAGATATGACAGCCGTCTACGCAACCCGACCCAGCGCT 1141
QY      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
      1142 GCTGCAGCGCGCGACCGGCTTACAGTATGACAGGTATAGCAGGTATGAGGTATACACAGCGGACCC 1201
QY      148  Tyr 148
      1202 TAC 1204

```

RESULT 5

```

US-09-974-300-1655
; Sequence 1655, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1655
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; NAME/KEY: misc_feature
; LOCATION: (1)-(657)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-1655

```

Alignment Scores:

```

Pred. No.: 0.0478 Length: 657
Score: 94.00 Matches: 38
Percent Similarity: 40.15% Conservative: 17
Best Local Similarity: 27.74% Mismatches: 58
Query Match: 11.81% Indels: 24
DB: 10 Gaps: 8

```

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-974-300-1655 (1-657)

OY 2 ThrAsnLysLysAlaLAsnProTyrThrAsnGlyThrValLeuAsnProValValGly 21
||| ||||| :||| ||| ||| |||||
Db 100 ACAAAAAAAAAACCAATTAAACCA---ACGAGGGCTTTAAAAAGCAAGCGGTAAACCTC 156

OY 22 -----AlaValTyrSerProAspPhe---TyrAlaGlyThrValLeuLeu 35
||| :||| ||||| |||
Db 157 TTAACCGCCCCCGGCTTTTCCAGAGATTCTTACAAACAAACCTGGGCTCCTT 216

OY 36 CysAlaAlaAsnGlnGlySerSerMetTyrSerGlyProSerSerLeuValTyrThr 55
:||||| ||||| |||
Db 217 ACCACCAAAAAAACAAGGTCGCGTTTC-----CCCTTAAGAAAAATTAAAC 267

OY 56 SerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGlyAla 75
||| ||| :||| ||||| |||||
Db 268 CCCCTTAACCAAAATTCACTTTTAACTTAAAGCGCAACCCCAACCCCAACCTC 327

OY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
||| :||| ||| :||| |||||
Db 328 CATATTTCATCTCTGGT-----TTCAAAATTTTTCATCATTAACCAACCCCG 378

OY 96 ProIleProAla-----TyrGlyGlyValValTyrGlnGlu 107
||| :||| ||| :||| |||||
Db 379 AAAAACCCCTCCCGGTACAACTTATTTTCAAAATACACAGGGGCTTGGCTGGGAA 438

OY 108 ProValTyrGlyAsnLysLeuGlnGly-----TyrAlaAlaTyr 122
||| :||| ||| :||| |||||
Db 439 CCAATTAACCAAC---CTGGCAAGGCGGCAAGGCTTACTCTCCTTAC 486

RESULT 6
US-10-027-632-24830
: Sequence 24830, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24830
: LENGTH: 699
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-24830

Alignment Scores:
Pred. No.: 0.0778 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 13 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-027-632-24830 (1-699)

OY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAla-AsnGlnGlySerse 44
:||||| ||||| ||| :|||
Db 84 ACACGACAGACAAAGGGGCTCAATCCCTCTGCTCTGCTTCA-----YCTGG 134

OY 44 rMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
||| ||||| ||||| |||
Db 135 ACAAGTCTCAGGCCCCAGCATCTC---CAGGAGACCAAGGCGCTGCTCTTACCA 191

OY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgGly 74
||| :||| ||||| |||
Db 192 CTGACCTCACCAGTCCCTCCCAAGTCCAGCTCCACCTCTCTCCTTCCCAAGAG 251

OY 74 yAlaHisLeuArgGlyArg----- 80
||| :||| |||
Db 252 AGAARACCTTAATACGAATCTCCAGGTGATGAGGTACAGATCTTGGCTCTCC 311

OY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
||| ||| ||| |||||
Db 312 TGTGCCCCCTGACCCGGGACACCTCTCCACGACCATGTCTGATGTCCCTCTCC 371

OY 95 oProIleProAlaTyrGlyGlyVal-----Val-TyrGlnGluProValTyrGlyAla 112
||| :||| ||||| |||||
Db 372 TCAGAGCCCTCTTACAGTGGGTCTCTGGAATGCTCTTCCCAACCATCTTACGAA 431

OY 112 snLys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
||| :||| ||| :||| |||||
Db 432 ATCTGCTCTTCCAGGC-----CCAGTCCAGCCCG 464

OY 132 Ala 132
|||
Db 465 GCA 467

RESULT 7
US-10-027-632-24831
: Sequence 24831, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24831
: LENGTH: 699
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-24831

Alignment Scores:
Pred. No.: 0.0778 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 13 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-027-632-24831 (1-699)

QY 25 SerProaspheTyraLaGlyThrValLeuLeuGlyGlnAla-AsnGlnGluGlySerse 44
:|||||
Db 84 ACACACACAGAACAGGGGCTCAATCCCTCTGCTGCTGCTCA-----YCTGG 134
QY 44 rMetTySerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyrr-- 63
:|||||
Db 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGNAGACCCAGGGGCTGCTGCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyraGgl 74
Db 192 CTGACCTCACCAAGTCCCTCCCAAGTCCAGCCTCCACCTCTCTCTGCCCCAGAG 251
QY 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTAAATCGAAATCTCCACGTGATAGAGTACAGAGTCTTGCCCTTCC 311
QY 81 -----GlyArgThrValTyraThrPheArgAlaAlaAlaProProp 95
Db 312 TGGTCCCCCTGACCCGGGCACACCTCTCCACAGCATGTCTGASATGTCCTCTCC 371
QY 95 oProLeProAlaTyrlGlyAla-----Val-TyrGlnGluProValTyrlGly 112
Db 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTGGAATGCTTCCCAACCATCTACGCCAA 431
QY 112 snlys-LeuLeuGlnGlyTyraAlaAlaTyraArgTyraAlaGlnProThrProAlaThr 131
Db 432 ATCTGCTCTTCCGAGGC-----CCAGTCCAGCCCG 464
QY 132 Ala 132
Db 465 GCA 467

RESULT 8

US-10-027-632-24832
: Sequence 24832, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027, 632
: PRIORITY FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24832
: LENGTH: 699
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-24832

Alignment Scores:

Pred. No.: 0.0778
Score: 92.50
Percent Similarity: 37.76%
Best Local Similarity: 28.67%
Query Match: 11.62%
13

Length: 699

Matches: 41

Conservative: 13

Mismatches: 41

Indels: 48

Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-027-632-24832 (1-699)

QY 25 SerProaspheTyraLaGlyThrValLeuLeuGlyGlnAla-AsnGlnGluGlySerse 44
:|||||
Db 84 ACACACACAGAACAGGGGCTCAATCCCTCTGCTGCTGCTCA-----YCTGG 134
QY 44 rMetTySerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyrr-- 63
:|||||
Db 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGNAGACCCAGGGGCTGCTGCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyraGgl 74
Db 192 CTGACCTCACCAAGTCCCTCCCAAGTCCAGCCTCCACCTCTCTCTGCCCCAGAG 251
QY 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTAAATCGAAATCTCCACGTGATAGAGTACAGAGTCTTGCCCTTCC 311
QY 81 -----GlyArgThrValTyraThrPheArgAlaAlaAlaProProp 95
Db 312 TGGTCCCCCTGACCCGGGCACACCTCTCCACAGCATGTCTGAGATGTCCTCTCC 371
QY 95 oProLeProAlaTyrlGlyAla-----Val-TyrGlnGluProValTyrlGly 112
Db 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTGGAATGCTTCCCAACCATCTACGCCAA 431
QY 112 snlys-LeuLeuGlnGlyTyraAlaAlaTyraArgTyraAlaGlnProThrProAlaThr 131
Db 432 ATCTGCTCTTCCGAGGC-----CCAGTCCAGCCCG 464
QY 132 Ala 132
Db 465 GCA 467

RESULT 9

US-10-301-822-25
: Sequence 25, Application US/10301822
: Publication No. US20030148410A1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Berger, Allison
: APPLICANT: Guillemette, Tracy L.
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Schlegel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Thibodeau, Stephen N.
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: TITLE OF INVENTION: THERAPY OF COLON CANCER
: FILE REFERENCE: MPN01-029P28NM
: CURRENT APPLICATION NUMBER: US/10/301,822
: PRIORITY FILING DATE: 2002-11-21
: PRIOR APPLICATION NUMBER: US 60/339,971
: PRIOR FILING DATE: 2001-12-10
: PRIOR APPLICATION NUMBER: US 60/361,978
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/381,988
: PRIOR FILING DATE: 2002-05-20
: NUMBER OF SEQ ID NOS: 228
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 25
: LENGTH: 11447
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(9192)
US-10-301-822-25

Alignment Scores:

Pred. No.: 2.46
Score: 92.50

Length: 11447

Matches: 28

Percent Similarity:	39.32%	Conservative:	11.12%
Best Local Similarity:	27.45%	Missed:	21.21%
Query Match:	11.62%	Indels:	2.21%
DB:	12	Gaps:	7%

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-301-822-25 (1-11447)

QY	50	SeSerLeuValAlaIYrThnSerAlaMetProGlyPheProAlaAlaThrAlaLa	69
Db	6232	AACAATGAATACTGCAGACCCCTGCACACTGCACACTCCAAAT	6288
QY	70	AlAlaIaIyArG-----GlyAlaAlaIaLeuArGlyArGlyArGThVal-----	84
Db	6289	GCTGTATTATGAAATGAGATGAGATGGCCACTTAACAGGAATGTGAAGAACTGGGACTC	6348
QY	85	-----TyrAsnThrPheArGAlaAlaLa	92
Db	6349	CTTCCTCCTCAGAACATACACATCTGTGACGAATGGTATGAAAGATTAGGGGTGTCTCG	6408
QY	93	ProProProProlIeProAlaTyrglyGlyValValTyrglnGluProValItyrGlyAsn	112
Db	6409	GATCTCTTCACCTTCTCCAGTCTTGGAAATAAATAGTAATTAAGCCAGTGGGTTCAT	6468
QY	113	LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgGlyTyrAlaGlnProThrPro	129
Db	6469	GAGCCCATGGAAGAGCTTGTGTGGAGAAATGACATCATATAGCTTAACACAAATCTCAATCC	6528
QY	130	AlAlaThr	131
Db	6529	AGCACG	6534

RESULT 10

US-10-177-293-60

Sequence 60, Application US/10177293

Publication No. US20030124128A1

GENERAL INFORMATION:

APPLICANT: Lilile, James
 APPLICANT: Glatz, Karen
 APPLICANT: Zhao, Xumel
 APPLICANT: Gannavarpu, Manjula
 APPLICANT: Kamathkar, Shubhangli
 APPLICANT: Mertens, Maureen
 APPLICANT: Myer, Vic
 APPLICANT: Wang, Youzhen
 APPLICANT: Xu, Yongyao
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Monahan, John
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Bast Jr., Robert C.
 APPLICANT: Hortobagyi, Gabriel N.
 APPLICANT: Pusztai, Lajos
 APPLICANT: Meric, Funda
 APPLICANT: Sahin, Aysegul
 APPLICANT: Mills, Gordon B.
 TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
 TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
 FILE REFERENCE: MRI-038
 CURRENT APPLICATION NUMBER: US/10/177,293
 CURRENT FILING DATE: 2002-06-21
 PRIOR APPLICATION NUMBER: US 60/299,887
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/301,572
 PRIOR FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: US 60/306,501
 PRIOR FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: US 60/325,002
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US 60/362,585
 PRIOR FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: US 60/xxx,xxx
 PRIOR FILING DATE: 2002-05-14
 NUMBER OF SEQ ID NOS: 506
 SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 60
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-60

```

Alignment Scores:

Pred. No.:	2.46	Length:	11447
Score:	92.50	Matches:	28
Percent Similarity:	39.22%	Conservative:	12
Best Local Similarity:	27.45%	Mismatches:	41
Query Match:	11.62%	Indels:	21
DB:	14	Gaps:	4

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-177-293-60 (1-11447)

OY	50	SerSerLeuValTYrThrIleSerAlaMetProGlyPheProTYrProAlaIleThAlaLa	69
Dd	6232	AACATATTAATTACTGCAGCCCCCTGCACCACTGACACTCCATTT-----AAATTAAGTGTATT	6288
OY	70	AlAlAlaTYrArg-----GlyAlaHisLeuArgGLyArgGLyArgThVal-----	84
Dd	6289	GCTGTATTATGAAGATGGAGATGGCGCCATCTAACAGGAATAAGAGAAGACTGTGGGACTC	6348
OY	85	-----TyraSnrThrPheArgAlaAlaLa	92
Dd	6349	CTTCCTCCCTCAGAACATATACCATCTCTGACGAATGGTATACAAATCTCAGGTTCTCTCG	6408
OY	93	ProProProAlaLeProAlaTYrGLyGLyValTYrGLnGLuProValTYrGLyAsn	112
Dd	6409	GATCCCTTCACCTCTCCAGTTCAGTGATATAAATTAAGTATATAAGCACAGTGGGTTCCAT	6468
OY	113	LysLeuLeuGln-----GLYGlyTYrAlaIleATyrArgTYrAlaGlnProThPro	129
Dd	6469	GAGGCCATGGAGAGCCTTTGTTGGAGAAATGACATCATATACCTTACACAATCTCAATCCC	6528
OY	130	AlaThr	131
Dd	6529	AGCACCC	6534

RESULT 11

US-10-177-293-62

Sequence 62, Application US/1017729

Publication No. US20030124128A1

GENERAL INFORMATION:

APPLICANT: Little, James
 APPLICANT: Gialt, Karen
 APPLICANT: Zhao, Xumei
 APPLICANT: Gannavarpu, Manjula
 APPLICANT: Kamatkar, Shubhangi
 APPLICANT: Mertens, Maureen
 APPLICANT: Myer, Vic
 APPLICANT: Wang, Youzhen
 APPLICANT: Xu, Yongyao
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Monahan, John
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Bast Jr., Robert C.
 APPLICANT: Hortobagyi, Gabriel N.
 APPLICANT: Puzstal, Lajos
 APPLICANT: Meric, Funda
 APPLICANT: Sahin, Aysegul
 APPLICANT: Mills, Gordon B.
 TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
 FILE REFERENCE: MRI -038
 CURRENT APPLICATION NUMBER: US/10/177,293
 CURRENT FILING DATE: 2002-06-21
 PRIOR APPLICATION NUMBER: US 60/299,887
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/301,572
 PRIOR FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: US 60/306,501

;; PRIOR FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: US 60/325,002
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US 60/362,585
;; PRIOR FILING DATE: 2002-03-05
;; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
;; PRIOR FILING DATE: 2002-05-14
;; NUMBER OF SEQ ID NOS: 506
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 62
;; LENGTH: 11560
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: 10981
;; OTHER INFORMATION: n = A,T,C or G
US-10-177-293-62

Alignment Scores:
Pred. No.: 2.49 Length: 11560
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21
Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-177-293-62 (1-11560)

OY 50 SerSerleuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThAlaAla 69
Db 6345 AACAAATGTAATACGACGCCCTGCACACCTGCACATCATAT---AAATTAAGTATT 6401
OY 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgThVal----- 84
Db 6402 GCTGTTATGAAAGATGAGATGATGTCGCATCTACAGAAATGGAAGAACTGTGGACATC 6461
OY 85 -----TyrAsnThrPheArgAlaAlaAla 92
Db 6462 CTTCCTCCTCAGAACATACACATCTGCAGCAATGATATACAAATTCAGGGTCTCTGG 6521
OY 93 ProProProProleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsn 112
Db 6522 GATCCTTACCTTCTCCAGTCTTGATATATAATAGTATATAAGCAGTGGTCCAAAT 6581
OY 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThPro 129
Db 6582 GAGCCCATGGAAGCCTTTGTTGGAAATGACATCATATACCTTACACAAATCTCAATCCC 6641
Y 130 AlaThr 131
Db 6642 AGCAC 6647

RESULT 12
US-10-198-846-11039
;; Sequence 11039, Application US/10198846
;; Publication No. US2003009974A1
;; GENERAL INFORMATION:
;; APPLICANT: Lillie, James
;; APPLICANT: Xu, Yongyao
;; APPLICANT: Wang, Youzhen
;; APPLICANT: Steinmann, Kathleen
;; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;; TITLE OF INVENTION: THERAPY OF BREAST CANCER
;; FILE REFERENCE: MRI-049
;; CURRENT APPLICATION NUMBER: US/10/198, 846
;; CURRENT FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/306,220
;; PRIOR FILING DATE: 2001-07-18
;; NUMBER OF SEQ ID NOS: 14084
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11039

;; LENGTH: 11657
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: 1, 2, 3, 4, 11656, 11657
;; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11039

Alignment Scores:
Pred. No.: 2.51 Length: 11657
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21
Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-198-846-11039 (1-11657)

OY 50 SerSerleuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThAlaAla 69
Db 6398 AACAAATGTAATACGACGCCCTGCACACCTGCACATCATAT---AAATTAAGTATT 6454
OY 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgThVal----- 84
Db 6455 GCTGTTATGAAAGATGAGATGATGTCGCATCTACAGAAATGGAAGAACTGTGGACATC 6514
OY 85 -----TyrAsnThrPheArgAlaAlaAla 92
Db 6515 CTTCCTCCTCAGAACATACACATCTGCAGCAATGATATACAAATTCAGGGTCTCTGG 6574
OY 93 ProProProProleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsn 112
Db 6575 GATCCTTACCTTCTCCAGTCTTGATATATAATAGTATATAAGCAGTGGTCCAAAT 6634
OY 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThPro 129
Db 6635 GAGCCCATGGAAGCCTTTGTTGGAAATGACATCATATACCTTACACAAATCTCAATCCC 6694
Y 130 AlaThr 131
Db 6695 AGCAC 6700

RESULT 13
US-09-996-634-62
;; Sequence 62, Application US/09996634
;; Patent No. US20020172684A1
;; GENERAL INFORMATION:
;; APPLICANT: Nano, Francis
;; APPLICANT: Mycobacterium Tuberculosis DNA Sequences Encoding
;; TITLE OF INVENTION: Immunostimulatory Peptides
;; TITLE OF INVENTION: Immunostimulatory Peptides
;; FILE REFERENCE: 61260
;; CURRENT APPLICATION NUMBER: US/09/996, 634
;; CURRENT FILING DATE: 2001-11-28
;; PRIOR APPLICATION NUMBER: 09/447,135
;; PRIOR FILING DATE: 2000-01-03
;; PRIOR APPLICATION NUMBER: 08/990,823
;; PRIOR FILING DATE: 1997-12-15
;; PRIOR APPLICATION NUMBER: US 96/10375
;; PRIOR FILING DATE: 1996-06-14
;; PRIOR APPLICATION NUMBER: 60/000,254
;; PRIOR FILING DATE: 1995-06-15
;; NUMBER OF SEQ ID NOS: 169
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 62
;; LENGTH: 821
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)-(821)
;; OTHER INFORMATION: n is a, c, g, or t/u.
US-09-996-634-62

; PRIOR FILING DATE: 1997-12-15
 ; PRIOR APPLICATION NUMBER: US 96/10375
 ; PRIOR FILING DATE: 1996-06-14
 ; PRIOR APPLICATION NUMBER: 60/000,254
 ; PRIOR FILING DATE: 1995-06-15
 ; NUMBER OF SEQ ID NOS: 169
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 62
 ; LENGTH: 821
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(821)
 ; OTHER INFORMATION: n is a, c, g, or t/u.
 US-09-997-181-62

Alignment Scores:

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US-09-809-545a-2_copy_1_148 (1-148) x US-09-997-181-62 (1-821)

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QY      41 GlnGlySerSerMetTyrSerGlyProSer-----SerLeuValTyr 54
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DB      190 AGGCGTGGGCGAGCACTCAAGTCCGAGCCGCGTCTCCCAACCGCGCGCTGCTCAAC 249
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QY      55 ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrArgGly 74
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DB      250 TCCGATCGCTGCCCAACCAACCAACCGCGCATCCGACTCCGCGGCGACCGCGCGGA 309
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QY      74 ----- 74
DB      310 GGGAGGCGCCGNTCCGATNCAACGGGTGCGACGGCGCTGCCCTTCNGATTGCA 369
      111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      75 -----AlaHisLeuArgGlyArg-----GlyArgThrValTyr 85
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DB      370 CCCGCGACGTACCCCGGTGATGGCGAGGAGGAGACAACTG3CCGCCACGGCGCAC 429
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DB      430 CTCGGCGCTGTACCACTACCGCCCGCAGCCCGCGCGCTGCTGCTGCTGCTGCTGCT 480
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QY      106 GlnGluProValTyrGlyAsnLys-----LeuLeuGlnGlyGly----- 118
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      111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      119 -----TyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
      111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      535 CGGCCAGTCCCTGAACCTGACAGGGGCGCTCAACCGCGCGCGCGCGCGCGCGCGCGCG 594
      111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      132 AlaAlaAlaTyrSerAspSerTyr 139
      111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      595 GGGGCGAGTATTCGATCGACAT 618
      111 111 111 111 111 111 111 111 111 111 111 111 111 111

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Search completed: September 25, 2003, 12:16:06
 Job time : 167 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: September 25, 2003, 11:50:55 ; Search time 275.5 Seconds
(without alignments)
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Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 566894 segs, 151307093 residues

Total number of hits satisfying chosen parameters: 1133788

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: Published.Applications_AA:*

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18: /cg2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	1086	93.3	203	US-09-809-545a-2	Sequence 2, Appl1
2	624	53.6	330	US-09-794-591-2	Sequence 2, Appl1
3	315.5	27.1	366	US-10-359-385-2	Sequence 2, Appl1
4	116	10.0	3063	US-10-301-822-26	Sequence 26, Appl
5	116	10.0	3063	US-10-177-293-61	Sequence 61, Appl
6	116	10.0	3063	US-10-177-293-61	Sequence 61, Appl
7	101.5	8.7	228	US-10-017-161-1348	Sequence 1348, Ap
8	99	8.5	919	US-10-128-714-8387	Sequence 8387, Ap
9	98.5	8.5	1168	US-09-919-603-2	Sequence 2, Appl
10	96.5	8.2	1302	US-09-935-384-764	Sequence 764, App
11	96	8.2	388	US-10-012-952A-172	Sequence 172, App
12	96	8.2	760	US-08-754-311B-2	Sequence 2, Appl1
13	95.5	8.2	168	US-09-864-761-40976	Sequence 40976, A
14	95.5	8.2	1172	US-09-919-770-4	Sequence 2, Appl1
15	95.5	8.2	1172	US-09-822-682-2	Sequence 2, Appl1
16	95.5	8.2	1172	US-10-301-822-203	Sequence 203, App
17	95.5	8.2	1172	US-10-008-093-4	Sequence 4, Appl1
18	95.5	8.2	1172	US-10-060-036-171	Sequence 171, App
19	95.5	8.2	1172	US-10-020-141-14	Sequence 14, Appl
20	95.5	8.2	1172	US-10-017-724-2	Sequence 2, Appl1
21	95	8.2	230	US-09-874-062-3	Sequence 3, Appl1
22	93.5	8.0	288	US-09-764-893-4903	Sequence 4903, Ap
23	93	8.0	692	US-10-156-761-14649	Sequence 14649, A
24	92	7.9	219	US-09-922-480-2	Sequence 2, Appl1
25	92	7.9	219	US-09-923-236-2	Sequence 2, Appl1
26	92	7.9	219	US-09-922-469-2	Sequence 2, Appl1
27	92	7.9	584	US-10-156-761-12405	Sequence 12405, A
28	92	7.9	2027	US-10-140-472-175	Sequence 175, App
29	92	7.9	2027	US-10-141-761-175	Sequence 175, App
30	92	7.9	2027	US-10-142-885-175	Sequence 175, App
31	92	7.9	2027	US-10-123-155-175	Sequence 175, App
32	92	7.9	2027	US-10-146-731-175	Sequence 175, App
33	90.5	7.8	481	US-10-156-761-12012	Sequence 2152, Ap
34	90.5	7.8	548	US-10-017-161-2152	Sequence 16, Appl
35	90.5	7.8	993	US-10-004-551-14	Sequence 1068, Ap
36	90.5	7.8	994	US-09-922-217-1068	Sequence 1068, Ap
37	90.5	7.8	5179	US-09-833-263-1068	Sequence 1068, Ap
38	90.5	7.8	5179	US-10-025-380-1068	Sequence 11221, A
39	90.5	7.7	342	US-10-156-761-11221	Sequence 7979, App
40	89.5	7.7	40	US-10-213-509-5	Sequence 5, Appl1
41	89.5	7.7	620	US-10-156-761-7979	Sequence 1067, App
42	89.5	7.6	219	US-09-746-877-1567	Sequence 1567, Ap
43	89	7.6	171	US-09-764-877-1567	Sequence 10205, A
44	88.5	7.6	363	US-10-156-761-10205	
45	88.5	7.6			

ALIGNMENTS

RESULT 1
US-09-809-545a-2
; Sequence 2, Application US/09809545A
; Patent NO. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS 017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-809-545a-2

Alignment Scores:

Pred. No.:	4	56e-89	length:	203
Score:	1086.00		Matches:	203
Percent Similarity:	100.00%		Conservative:	0
Best Local Similarity:	100.00%		Mismatches:	0

Query Match: 93.30% Indels: 0
DB: 10 Gaps: 0
US-09-809-545a-1_copy_535_1143 (1-609) x US-09-809-545a-2 (1-203)

QY 1 ATGACTAATAAAGCCGCTACACCAATGCTGGAATTAATTCAGTTGTG 60
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QY 61 GCGCGGTCTACAGCCCGCACTTCTATGAGGAGGAGGTGTTGGCAGGCCAACCAG 120
DB 21 GlyAlaValIlyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyGlnAlaAsnGln 40
QY 121 GAGGAGATCTTCATGATAGTGGCCCACTTCTATGATTAATTAATTCAGTTGTG 180
DB 41 GluGlySerSerMetTyrSerCylProSerSerLeuValIlyrThrSerAlaMetProGly 60
QY 181 TTTCCATATCCGGCGCCGCACTGCTCAGACTGCATACCGAGGGGCTCAGAGCCGT 240
DB 61 PheProTyrProAlaAlaThrAlaAlaAlaIlyrAlaGlyAlaAlaIleuAlaTrg 80
QY 241 GGTGCACCGGTGTACACACCTTTCAGAGCTGGCGGCCCGCCCAATCCGCGCTAT 300
DB 81 GlyArgThrValIlyrAsnThrPheArgAlaAlaAlaProProProIleProAlaIlyr 100
QY 301 GCGCGAGTAGTGTATCAAGAGCCAGCTGTATGGCAATAATGCTACAGGGTGTACGCT 360
DB 101 GlyGlyValIlyrValGlnGluProValIlyrGlyAsnLysLeuLeuGlnGlyIlyrAla 120
QY 361 GCATACCGCTACGCCAGCCCGCCCACTGCTGCTGCTACAGTACAGTACGGA 420
DB 121 AlAllyrAlGlyrAlaGlnProThrProAlaThrAlaAlaIlyrSerAspSerTyrGly 140
QY 421 CGAGTTATGCTGCGCAGCCCTTACACACACACTTGTCTCCAGGCCCGCCAGTACGCGTT 480
DB 141 ArgValIlyrAlaAlaAspProTyrThrIshIshThrLeuAlaProAlaProThrIlyrGlyAl 160
QY 481 GGTGCATGAATGCTTTTGGCGCCCTTGACCCGATGCCAAGACTAGAGCCATGCTGATGAT 540
DB 161 GlyAlaMetAlaAlaPheAlaProLeuThrAspAlaIlyrThrArgSerHisAlaAsp 180
QY 541 GTGGGTCGTTCTTTCATGAGGCTAGTATATCCAAAGGGGATACAAACGCTTT 600
DB 181 ValGlyLeuValIleuSerSerLeuGlnAlaSerIlyrGlnGlyIlyrAsnArgPhe 200
QY 601 GCTCCATAT 609
DB 201 AlaProTyr 203

RESULT 2
US-09-794-591-2
; Sequence 2, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/145,391
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-591-2

Alignment Scores: 1.36e-47 Length: 330
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Percent Similarity: 89.78% Conservative: 4
Best Local Similarity: 86.86% Mismatches: 12
Query Match: 53.61% Indels: 2
DB: 9 Gaps: 0
US-09-809-545a-1_copy_535_1143 (1-609) x US-09-794-591-2 (1-330)

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QY 61 GCGCGGTCTACAGCCCGCACTTCTATGAGGAGGAGGTGTTGGCAGGCCAACCAG 120
DB 216 GlyAlaValIlyrSerProGluPheTyrAlaGlyThrValLeuLeuGlyGlnAlaAsnGln 235
QY 121 GAGGAGATCTTCATGATAGTGGCCCACTTCTATGATTAATTAATTCAGTTGTG 180
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QY 241 GGTGCACCGGTGTACACACCTTTCAGAGCTGGCGGCCCGCCCAATCCGCGCTAT 300
DB 276 GlyArgThrValIlyrAsnThrPheArgAlaAlaAlaProProProIleProAlaIlyr 295
QY 301 GCGCGAGTAGTGTATCAAGAGCCAGCTGTATGGCAATAATGCTACAGGGTGTACGCT 360
DB 296 GlyGlyValIlyrValIlyrProGlyTrpIleuThrProCysAlaGlnIleu--TrpIleuGlySc 315
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DB 315 yAlleProLeuAlaProAlaIlyrProCysHisCysArgCylLeuGln 330

RESULT 3
US-10-359-385-2
; Sequence 2, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-2

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Percent Similarity: 42.86% Mismatches: 59
Best Local Similarity: 27.10% Indels: 48
Query Match: 12 Gaps: 10
DB: 10

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QY	210	GlyAlaValTyrGlyProGluLeuTyrAlaAlaSerSerPheGlnAlaAspAlaSerLeu	229
Db	118	---CAGAGGGATCTTCATGTACAGTGGCCCCCACTACTT-----GTATATACTTCT	168
Db	230	GlyAsnAspAlaAlaValProLeuSerGlyArgGlyIleAsnThrTyrIleProLeu	249
QY	169	GCAATGCGCTGCTTCCATATCCG---GCCGCCACTGCTGCAGCTGCATATCCAGAGGCT	225
Db	250	IleIleProGlyPheProTyrProThrAlaAlaThrThrAlaAlaAlaPheArgGlyAla	269
QY	226	CACCTTGAGCGCGGTGTGCACCGCTGTAACAACACTTCAGAGCTTCGGCGGCCACCC	285
Db	270	HisLeuArgGlyArgGlyArgThrValTyrGlyAlaValArg---AlaValProProThr	288
QY	286	CCAATCCCGCGCTATGGCGAGTGTGTATCAAGACCGCAGTGTATGGCAATTAATGGTA	345
Db	289	AlaIleProAlaTyrProGlyAlaAspMetGln---ProThrAspMetHisSerLeuLeu	307
QY	346	CAGGTGGTTACGCTGCATACCGCTACAGCCCAACCCCACTGCATGCTGCTGCT--	403
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QY	404	-----ACAGTACAGTTACGAGAGAGATTATGCTGCCGACCCCTACACACACACA	453
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QY	454	CTTGCTCCAGCCCCCACTACGCGCTGTGTGCATGATGCTTTTSCCCCTTGACCGCAT	513
Db	336	-----MetProLeuProLeu	340
QY	514	GCCAGACTACGAGCCATGCTGATGATGTGGTCTCGTTCTTTCATTCAGAGCTAGT	573
Db	340	uPro---LeuAlaMetGluLeuAlaLeuTrp-----ArgVal	351
QY	574	ATATACCAAGGGGATACACACCGTTTG 601	
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RESULT 4			
US-10-301-822-26			
Sequence 26, Application US/10301822			
Publication No. US20030148410A1			
GENERAL INFORMATION:			
APPLICANT: Millennium Pharmaceuticals, Inc.			
APPLICANT: Berger, Allison			
APPLICANT: Guillemette, Tracy L.			
APPLICANT: Kamatkar, Shubhangi			
APPLICANT: Schlegel, Robert			
APPLICANT: Monahan, John E.			
APPLICANT: Thibodeau, Stephen N.			
APPLICANT: Burgart, Lawrence J.			
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND			
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND			
FILE REFERENCE: MP01-029P2RMN			
CURRENT APPLICATION NUMBER: US/10/301,822			
CURRENT FILING DATE: 2002-11-21			
PRIOR APPLICATION NUMBER: US 60/339, 971			
PRIOR FILING DATE: 2001-12-10			
PRIOR APPLICATION NUMBER: US 60/361, 978			
PRIOR FILING DATE: 2002-03-05			
PRIOR APPLICATION NUMBER: US 60/381, 988			
PRIOR FILING DATE: 2002-05-20			
NUMBER OF SEQ ID NOS: 228			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 26			
LENGTH: 3063			

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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-26

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Score: 116.00 Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best local Similarity: 25.14% Mismatches: 54
Query Match: 9.97% Indels: 64
DB: 12 Gaps: 8

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QY	208	GCTGCATACCGA-----GGGCGTCACCTTCGAGCGCGGTGCACCGTg-----	252
Db	2097	AlaValTyrGlnAspGlyAspGlyGlnHisLeuThrGlnAspGlnYArgThrValIleu	2116
QY	253	-----TACAACTTCAGAGCGCGCGG	276
Db	2117	LeuProProGlnAsnIleHisIleSerAspGluThrPyrThrArgPheArgValSerTyr	2136
QY	277	CCCCACCCCAATCCCGCGCCCTATGCGGAGTAGTGTATCAAGAGCCAGTATGACAT	336
Db	2137	AspProSerProSerProValLeuGlnTyrTyrIleValTyrTyrProValGlySerAsn	2156
QY	337	AAATGCTACAG-----GGTGGTTCACCTGCATACCGCTACGCCACCCACCCCT	387
		GluPromeGlnAlaPheValGlyGluMetThrSerTyrThrIleu-----	2171
QY	388	GCCACTGCTGTGCTACAGTACGACAGTTACGAGAGATTATGCTGCCGACCCCTACAC	447
Db	2171	-----	2171
QY	448	CACACACTGCTGCAGCGCCCGACCTACGGCGTGGTCGATGAATGCTTTTGCg-----	501
Db	2172	HisAsnLeuAsnProSerThrThrTyrAspVal-----AsnValTyrAlaGlnTyr	2188
QY	502	-----CCCTTACCGCATGCCAAGACTAGAGACCATGCTGATGATGTCG	543
Db	2189	AspSerGlyLeuSerValProLeuThrAspGlnGlyThr-----	2202
QY	544	GGTCTGCTCTCTTTTATTGACAGCTAGTATATACCAAGGGGAGATACACGCTTTT	600
Db	2203	---LeuTyrLeuAsnValThrAspLeuLysThrTyrGlnIleGlyTrpAspThrPhe	2220
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US-10-177-293-61			
: Sequence 61, Application US/10177293			
: Publication No. US20030124128A1			
: GENERAL INFORMATION:			
: APPLICANT: Lillie, James			
: APPLICANT: Glatz, Karen			
: APPLICANT: Zhao, Xumei			
: APPLICANT: Gannavarpu, Manjula			
: APPLICANT: Kamalakar, ShubhangI			
: APPLICANT: Mertens, Maureen			
: APPLICANT: Myer, Vic			
: APPLICANT: Wang, Youzhen			
: APPLICANT: Xu, Yongyao			
: APPLICANT: Hoersch, Sebastian			
: APPLICANT: Monahan, John			
: APPLICANT: Meyers, Rachel E.			
: APPLICANT: Bast Jr., Robert C.			
: APPLICANT: Hortobagyi, Gabriel N.			
: APPLICANT: Pusztai, Lajos			
: APPLICANT: Meric, Funda			
: APPLICANT: Sahlin, Aysegul			
: APPLICANT: Mills, Gordon B.			

```

: TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
: FILE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
: FILE REFERENCE: MRI-038
: CURRENT APPLICATION NUMBER: US/10/177,293
: PRIOR FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: US 60/299,887
: PRIOR FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: US 60/301,572
: PRIOR FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: US 60/306,501
: PRIOR FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: US 60/325,002
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US 60/362,585
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/xxx,xxx
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 506
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 61
: LENGTH: 3063
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-177-293-61

Alignment Scores:
Pred. No.:      0.0724      Length:      3063
Score:          116.00      Matches:     45
Percent Similarity: 34.08%   Conservative: 16
Best Local Similarity: 25.14% Mismatches:    54
Query Match:     9.97%       Indels:      64
DB:              15         gaps:        8

US-09-809-545A-1_COPY_535_1143 (1-609) x US-10-177-293-61 (1-3063)
Oy      148 AGCTGACTGTATATACCTTCTGCAGATGCGTGTCGTTCCATATCCGGCGCGCGCTGTGCA 207
Db      2078 AAnaAnValIleLeuInProLeuGlInProAsPrhrProLyr---LysIleThValIlle 2096
Oy      208 GCTGCATACC GA-----GGGGCTACCTTTCGAGGCCGTGGTCCGACCGCTG----- 252
Db      2097 AlAvalTyGrGluaRpclYaSrGlYglnIstleuthGrGlYasnGlYatGrThValIGlYeu 2116
Oy      253 -----TACAACACCTTCAGAGCGGGCG 276
Db      2117 LeuPProGInAsnIlehtIsIseSerAsRclUptTrlyThrArpHeAtYalSerTrp 2136
Oy      277 CCCCCACCCC CAATCCCGGCGCTATGGCGGAGTAGTGTATGCAAGCCAGTGTATGCAAT 336
Db      2137 AsPrroSerProserProvalLeuglYtyrLYslleValTYlYlsProvalGLyserAsn 2156
Oy      337 AAATTGCTACG-----GGTGGTACGCGTCATACCGCGTACGCCACCCACCCCT 387
Db      2157 GIuPPromEGgluaIdarheValIGlYImetThSerTrYrThrlEu----- 2171
Oy      388 GCCACTGCTGCTGCTCATAGTGAAGTACAGTACGAGAGATTATGCTGCCGACCCCTACAC 447
Db      2171 ----- 2171
Oy      448 CACACACTTGTCTCCACCCCGCACCTACGCGGCTTGCGCATGAATGCTTTTGG----- 501
Db      2172 HIsAsnLeuAsnProserThrThrTYrAsPVal1-----AsnValTYrAlagIntYr 2188
Oy      502 -----CCCTGACGAGATGCCAACAGCTAGAGCCATGCGATGATGATG 543
Db      2189 AsPserGlyLeuSerValProleuThAsRGlncIgIyrThr----- 2202
Oy      544 GGCTCGTCTTCTTCTTCATTTGACGGCTAGATATACCAAGGCGGATACACACCGTTTT 600
Db      2203 ---LeuTYrLeuAsnValThrAsRleuLYtThrTYrcInIleGIYTTPAsPrThrPhe 2220

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: Sequence_63 Application US/10177293
: Publication No. US20030124128A1
: GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Glatte, Karen
: APPLICANT: Zhao, Xumei
: APPLICANT: Ganavevarpu, Manjula
: APPLICANT: Kamatkar, ShubhangI
: APPLICANT: Mertens, Maureen
: APPLICANT: Myer, VIC
: APPLICANT: Wang, Youzhen
: APPLICANT: Xu, Yongyao
: APPLICANT: Hoersch, Sebastian
: APPLICANT: Moohan, John
: APPLICANT: Meyers, Rachel E.
: APPLICANT: Bast Jr., Robert C.
: APPLICANT: Horobagyl, Gabriel N.
: APPLICANT: Pusztai, Lajos
: APPLICANT: Meric, Funda
: APPLICANT: Sahin, Aysegül
: APPLICANT: Mills, Gordon B.
: TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
: FILE REFERENCE: MRI-038
: CURRENT FILING DATE: US/10/177,293
: PRIOR APPLICATION NUMBER: US 60/299,887
: PRIOR FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: US 60/301,572
: PRIOR FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: US 60/306,501
: PRIOR FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: US 60/325,002
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US 60/362,585
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/xxx,xxx
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 506
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 63
: LENGTH: 3063
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-177-293-63

Alignment Scores:
Pred. No.:          0.0724      Length:       3063
Score:              116.00      Matches:     45
Percent Similarity: 34.08%      Conservative: 16
Best Local Similarity: 25.14%   Mismatches: 54
Query Match:        9.97%       Indels:      64
DB:                 15         Gaps:        8

US-09-809-545A-1_COPY_535_1143 (1-609) x US-10-177-293-63 (1-3063)
QY    148 AGTTCACCTGTATTAAGTTGCGCATGGCCTTGCCGATGCAGGCGGCCGCAATGTGCA 207
      :*****:                |||||            |||
Db    2078 AsmnsvalilleuglnProleugInPrmsphrProtYr---LysIlcthvallile 2096
QY    208 GCTGCATPACGA-----GGGGCTCACCTTGAGGCGCGGTGTCACCGTg----- 252
      ||| |||               ||| ||||| ||| |||||||||
Db    2097 AlavalTyrglUAspglyAspglyGlyHlsIeurthrGlYngslYAgfThValIgLYeu 2116
QY    253 -----TACAACACTTCACAGAGCTGGCGGC 276
      :||| |             ||| ||||| :|||
Db    2117 LeuPProglInsIIeHIsIleseraSpGIuTPryTrHraGrpheayuaISetTp 2136
QY    277 CCCCAACCCCAGATCCGGCGCTATGGCGAGTAGTATCAAGAAGCGATGATGCAAT 236
      ||| ||| |||           ||| :||| ||||| |||
Db    2137 AspProSerProserProvaIleugLItyrlYlsIleValtyrlYrsProvalIGlySerAn 2156
QY    337 AAATYGCTACAG-----GGTGGTtTACCGTCAATACCgGTAPAGGCCAGCCACCCCT 387

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Db      117 GlnGlnPhgGIyAlamEtGIyAlThrsAsPro-----HisLseMetProPro-GInPr 134
OY      469 ACCTACGGGGTGTGCATGAATGCTTTTGCGCCCTTGAGCAGGCCAAGACTA 523
Db      134 oPFGInAlAlAlAlValAlAlAProGInAlAlAProKArgProValProLeuAnsGInleu 152

RESULT 9
US-09-919-603-2
: Sequence 2, Application US/09919603
: Patent No. US20020137679A1
GENERAL INFORMATION:
APPLICANT: Lawler, John W.
TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TSP
FILE REFERENCE: 1440.1033-007
CURRENT APPLICATION NUMBER: US/09/919, 603
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: PCT/US00/02482
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/118, 053
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1168
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-603-2

Alignment Scores:
Pred. No.:          2.28           Length:         1168
Score:              98.50           Matches:         50
Percent Similarity: 35.55%          Conservative:    25
Best Local Similarity: 23.70%       Mismatches:     66
Query Match:        8.46%           Indels:         71
DB:                 10              Gaps:           13

US-09-809-545A-1_COPY_535_1143 (1-609) x US-09-919-603-2 (1-1168)
OY      12 AAGGCGGTGAACCCTTACCAATGCTGGAATAATTAATTCAGTGTGGCGCGGTCTA 71
Db      380 GGIIIGIITPSePrOTrpAlaGluTrpPhrGIncysSerValThrCysGlSerglyThr 399
OY      72 CAGCCCCGAGCT-----TGTCACAGGCCAACAGAGAGCAT-----TGTATGCAG 91
Db      400 GInGlnArGIyArgSerCysAspValThrSerAnthrCysLeuGlyProserIleGln 419
OY      92 GCAGCGTGTCT-----TGTCACAGGCCAACAGAGAGCAT-----127
Db      420 ThrArgAlacSerIeuSerIeuCysAspHrArgIleatGlnAspGlyTyTPser 439
OY      128 -----CTTCATGTACAGTGGCGCCAGTTCACTTGAT 160
Db      440 HisTPSePrOTrpSeSerCysSerValThrCysGlyAlaGlyAsnIle-ThrArgIl 459
OY      161 ATACTTGTGCAATGCTGGCT---TCCATATCGCGCGCACGTGCAGTGCATACC 217
Db      459 eArGleuNysAnsSerProValProGlnMeclGIyLyAsnIeCs-----474
OY      218 GAGGGCTTACCTTGAAGCGGTGTGSCACCGTGTACAACACCTTGAGAGCTGC--66 274
Db      475 -lysGlySerGly-----ArgIuThrLySalCysGInGI 486
OY      275 CGCCCCAACCCCAATCCCGGCTATGGCGGAGTAGTGATCAAGAACCGATTATGGCA 334
Db      486 yAlaProCysProlIeaSpGIyAlhytTP-----SerProtrp-- 498
OY      335 ATAAATGCTACAGGGGTGTACGCTGCATACCCCTACGCCACGCCACCCCTGCCACTG 394
Db      499 -----SerProtrPserAlaCysFhlVal-----Th 507
OY      395 CTGCTGCTTACAGTAGTACGAGAGGTTTATGCTGCCGACCCCTACCACCAAC-- 452

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[illegible]


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Db      367 yscysCysAlaCys-ThnCysAlaThrAlaCysCysAlaGlyCysCysAlaCys 384
RESULT 11
US-10-012-952A-172
; Sequence 172, Application US/10012952A
; Publication No. US20030175707A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve.
; APPLICANT: Chen, Sel-Yu
; TITLE OF INVENTION: Composition and Methods Relating to Prostate Specific Genes and F
; FILE REFERENCE: DEX-0263.
; CURRENT APPLICATION NUMBER: US/10/012,952A
; PRIORITY FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/246,039
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-952A-172

Alignment Scores:
Pred. No.:      3.18      Length:      388
Score:          96.00     Matches:      59
Percent Similarity: 31.65%  Conservative: 16
Best Local Similarity: 24.89%  Mismatches: 86
Query Match:      8.25%     Indels:      76
                        Gaps:      11
DB: 12

US-09-809-545a-1_COPY_535_1143 (1-609) x US-10-012-952A-172 (1-388)
QY      61 GGGCGGCTTACAGCCCCGAGCTTATGACGAGCAGCGTGTGCGCAGCCAG 120
      111 :::111 :111
Db      67 Gly1GlyasnPheserValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 86
QY      121 GAGGAGCTTCCATGATGAGCGGCCCACTGTCATCTT-----GTATAT 162
      ::::111 :111
Db      87 ---CysArgasnLeuMetAlaHisProAlaProLeuAlaProGlyAlaAlaSerAla 105
      ::::111 :111
QY      163 ACTTGTGCATGCTGCTGCTTCCATATCCGGCCGCACTGTCGCACTGTCATACCGAGG 222
      ::::111 :111
Db      106 SerSerAla---ProGlyGlyAlaProProSerAlaAlaAlaAlaAlaAla 124
      ::::111 :111
QY      223 GCTACCTTGCAGGCGCTGTCGACCGGTGTAACAACCTTCAGAGCTGCGGCCGCCCA 282
      ::::111 :111
Db      125 Ala-----AlaAlaAlaAlaAlaAlaAlaAlaAlaSerSerGlyProGly 140
      ::::111 :111
QY      283 CCCCCAATCCCGGCTATGGCGGAGTAGTATCA----- 318
      ::::111 :111
Db      141 ProAlaGlyProAlaGlyAlaGlyAlaAlaLysGlnCysSerProCysSerAlaAla 160
      ::::111 :111
QY      319 GAGCCAGTGTATGCAATTAATTGCTACAGGGGTGATACCGTACCGCTAC----- 372
      ::::111 :111
Db      161 GlnSerSerSerGlyProAlaAlaLeuProGlyTrpGlyTrpGlySerGlyTyrTyrPro 180
      ::::111 :111
QY      373 -----GCCAAGCCCAACCCCTGCC 390
      ::::111 :111
Db      181 CysAlaArgMetGlyProHisProAsnAlaLeuLysSerCysAlaGlnProAlaSerAla 200
      ::::111 :111
QY      391 ACTGCTGCTGCC-----TACAGTACAGCT----- 414
      ::::111 :111
Db      201 AlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 220
      ::::111 :111
QY      415 -----TACGACGAGTTTATGCTGCGCCGACCTAC 444
      ::::111 :111
Db      221 PheSerSerArgAlaLysGlnPheAlaPheTyrHisGlnGlyTyrAlaAlaGlyProTyr 240
      ::::111 :111
QY      445 CACCACACACTTGTCTCAGGCCGCCACCTAC-----GGCGTGTGT 483
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Db      241 HisHisHis---GlnProMetProGlyTyrLeuAspMetProValProGlyLeuGly 259
QY      484 GCCATGATGCTTTTGGCCCTTACCGATGCCAAGACTAGAGCCCATGCTGATGATG 543
Db      260 GlyProGly-----GlnSerArgHisGlnProLeu 269
QY      544 GGCTCGTCTTCTTCTTCATTCAGAGCTATATACCAAGGCGGATCAAC 594
      ::::111 :111
Db      270 GlyLeuProMetGlnSerTyrGlnProTyrAlaLeuProAsnGlyTyrPasn 286
      ::::111 :111
RESULT 12
US-08-754-311B-2
; Sequence 2, Application US/08754311B
; Publication No. US20020004221A1
; GENERAL INFORMATION:
; APPLICANT: Bonini, Nancy M.
; APPLICANT: Leiserson, William M.
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Holbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/754,311B
; FILING DATE: 21-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/195,152
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccarlin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-59551/RET/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 760 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-754-311B-2

Alignment Scores:
Pred. No.:      3.56      Length:      760
Score:          96.00     Matches:      42
Percent Similarity: 37.29%  Conservative: 24
Best Local Similarity: 23.73%  Mismatches: 61
Query Match:      8.25%     Indels:      50
                        Gaps:      6
DB: 6

US-09-809-545a-1_COPY_535_1143 (1-609) x US-08-754-311B-2 (1-760)
QY      124 GGATCTTCATGATAC-----AGTGGCCCGAGTTCATT 156
      ::::111 :111
Db      223 GlySerAsnLeuTyrGlyCysSerSerAlaSerAsnProLeuAspGlyAlaValAla 242
      ::::111 :111
QY      157 GTATATACCTTGCATATGCTGCTTCCATATATCCGGCCGCACTGTCGACGTGATAC 216
      ::::111 :111
Db      243 ValAsnSerSerAlaVal-----AlaAlaAlaAlaAlaAlaValTyr 256
      ::::111 :111

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OY 217 CGAGGGCTACACCTTCGAGCGCGTGTGTCACCGTGTACACACCTTCGAGCGCGG 276
    ||| |||
Db 257 ASRGLYLGNHs-----AspTYTYTYTYAsnSerMetGlnGlnTYrThr 272
OY 277 CCCCCACCCCAATCCCGGCTATGGCGGAGTAGTATCAAGACCCAGCTGATGGCAAT 336
    ||||| |||||
Db 273 PropioPhenTySerGlyTYrGlyThrProTYrAlaAlaAlaThrAlaAlaArgGln 292
OY 337 AATATGCTACAGGAGGTACCGTGCATACCGCTACGCGACGCCCGCTGCACTGCT 396
    ||||| |||||
Db 293 AlaLysMetGlnProGlyAlaAlaAlaAlaAlaAlaTYrLeuThrProSerTYrAla 312
OY 397 GCTGCC----- 402
    |||||
Db 313 AlaSerGlyAsnAsnAsnSerGlnLeuTYrSerSerProTYrAlaGlyTYrAsnAsn 332
OY 403 -----TACAGTACAGTACAGGACGAGCTTATGCTGCCGAC 438
    ||||| |||||
Db 333 GlyGlnGlnAspTYrGlyGlyTYrTYrAsnGlnGlnTYrGlyAsnTYrTYrSerProAla 352
    ||| |||||
OY 439 CCTACACACACACACTTCTGCTCCAGCGCCC-----ACCTACGCGGTGGT--- 483
    ||| |||||
Db 353 AsnTYrSerProTYrAlaAlaAlaSerSerProSerSerSerAlaSerHisGlyPhe 372
OY 484 GCCATGATGCTTTGGCGCCCTGACCGATGCCAAGCTAGAGCCATGCT 534
    ||| ||| ||| ||||| ||| |||||
Db 373 HisValAlaAlaSerSerAsnLeuSerGlnSerProThrAspThrHisSer 389

RESULT 13
US-09-864-761-40976
; Sequence 40976, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40976
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011815.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EST HUMAN HIT: T70393.1, EVALU 5.00e-17
; OTHER INFORMATION: SWISSPROT HIT: P31794, EVALU 2.10e-01
US-09-864-761-40976

Alignment Scores:
Pred. No.: 3.06 Length: 168
Score: 95.50 Matches: 42
Percent Similarity: 35.22% Conservative: 14
Best Local Similarity: 26.42% Mismatches: 50
Query Match: 8.20% Indels: 53
DB: Gaps: 11

US-09-809-545A-1_COPY_535_1143 (1-609) x US-09-864-761-40976 (1-168)
OY 15 GCCCGTGAACCCCTACACCAATGCTGCAATTTAA-----TCCAGTGTGGCGCG 65
    ||| ||||| ||||| |||||
Db 8 GlyProGlnProGlnProGlyTyrPheGlnHisLysGlyGlyGlyCysArgGly 27
OY 66 GGT-----CTACAGCGCCGACTTCTATGACAGCAGCGTGTGTGCCAGCGCA 116
    ||| ||||| ||||| |||||
Db 28 GlySerCysLeuLeuGlnHisSerCysLeuLeuTrpHisSerCysLeuLeuProAlaSer 47
OY 117 CCAGAGGAGATCTTCATGATGACAGTGGCCCGCATTCCTATGATTAATTCGATAGCC 176
    ||| |||||
Db 48 LysAsnThrVal-----CysSerLys 54
OY 177 TGGCTTTCATATCCGGCCGCGCAGTGTGACACTGCTATACCGAGGGC---TCACCTTCG 233
    ||| |||||
Db 55 -----AspLeuGlyGly-----CysSerCysThrGlnGlnSerArgAlaProAla 69
OY 234 AGCGCGTGTGCGACCGGTACAA-----CACCTTCAGAGCTGC 272
    ||||| ||| |||
Db 70 CysSerTrpSerProArgThrGlnGlnGlySerAlaSerSerHisAspLeuLysCys 89
OY 273 -----GGCGCCCGCCACCCCAATCCGGC----- 296
    ||||| ||||| |||||
Db 90 SerTYrAlaTrpGlyAlaProThrArgGlnLeuGlyArgSerTrpAlaProAlaCysPro 109
OY 297 -----CTATGG-----CGAGTAGTGTATCAAGACCGCAGTGTATGCAATTAAT 341
    ||||| ||||| ||||| |||||
Db 110 ArgSerLeuTrpLeuCysGlnAlaHisSerMetGlyArgAlaSerTrpLeuGlnProAla 129
OY 342 GCTACAGGCGGTGCTACGCTGATACCGCTACCGCCAGCCACCCCTGCACACTGCTGC 398
    ||| ||||| |||||
Db 130 SerTrpGlnTrp-----ProLeuGlnMetValGlnMetAlaHisCysCys 144

RESULT 14
US-09-919-770-4
; Sequence 4, Application US/09919770
; Patent No. US20020048577A1
; GENERAL INFORMATION:

```

APPLICANT: Bornstein, Paul
APPLICANT: Kyriakides, Themis
APPLICANT: Ratner, Buddy
APPLICANT: Giachelli, Cecilia
APPLICANT: Martinson, Laura
APPLICANT: Scatena, Maria
TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
FILE REFERENCE: US09/117618
CURRENT APPLICATION NUMBER: US/09/919,770
PRIORITY FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,071
PRIORITY FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent version 3.0
SEQ ID NO 4
LENGTH: 1172
TYPE: PRN
ORGANISM: Homo Sapien
US-09-919-770-4

Alignment Scores:

Pred. No.:	4.25	Length:	1172
Score:	95.50	Matches:	50
Percent Similarity:	35.55%	Conservative:	25
Best Local Similarity:	23.70%	Mismatches:	66
Query Match:	8.20%	Indels:	71
DB:	9	Gaps:	13

US-09-809-545a-1_COPY_535_1143 (1-609) x US-09-919-770-4 (1-1172)

QY 12 AAGGCGGTGACCCCTACACCAATGCTGGAATTAATTCAGTTGTGGCGGCTCTA 71
Db 382 GlnuIlyrprserProtrpalaGluTrpThrcIncysserValThrcysglYserGlyThr 401
QY 72 CAGCCCGGACT-----TGTCCAGGCCAACAGAGGAT-----TCTATGACAG 91
Db 402 GlnuIlyrprserProtrpalaGluTrpThrcIncysserValThrcysglYserGlyThr 421
QY 92 GCACGGTGTGT-----TGTCCAGGCCAACAGAGGAT-----TCTATGACAG 127
Db 422 ThrArgAlacysSerLeuSerLysCysAspThrArgIleArgGlnAspGlyYTrpSer 441
QY 128 -----CTTCATGTCACAGTGGCCCGGACCTGTCACAGTTCATGTCAT 160
Db 442 HistPrserProtrpserSerCysSerValThrcysglYalGlyAsnIle-ThrArgIl 461
QY 161 ATACTTGCATAGCTGCTT---TCCATATCCGCGCCGACCTGTCACAGTTCATGTCAT 217
Db 461 eArgLeucYsaSnsrProvalProGlnMeIglYlYsaSncys----- 476
QY 218 GAGGGCTCACCTTCGAGGCCGTGTGCGACCGGTGTACACACCTTCAGAGCTGC--GG 274
Db 477 -LysGlySerGly-----ArgGlnuThrLysAlacysGlnG 488
QY 275 CGCCCCCAACCCCAATCCCGGCTATGGCGGAGTAGTATCAAGAAGCAGTGTATGCA 334
Db 488 yAlaProCysProIleAspIlyArgTrp-----SerProtrp-- 500
QY 335 ATAAATTGTCACAGGTGTTAGCGATACCGCTACGCCACCCACCCCTGCCACTG 394
Db 501 -----SerProtrpserAlacysThVal-----Th 509
QY 395 CTGCTGCTACAGTACGAGAGTATTAGTGTGCGACCCCTACACACACAC-- 452
Db 509 rcysAlaGlylYleArgIleArgGlnuArgThrArgValCysAsnsrProGlnuProGlnuYrgl 529
QY 453 -----ACTTGC---TCCAGCCCCCAGCTACGGCGGTGGCGCATATGCTTTTGGCG 502
Db 529 yGlyLysAlacysValGlyAspValGlnuArgGlnMeCysAsnLysArgSerCysPr 549
QY 503 CCTTGACCGGACCAAGACTAGAGCCATGC 533
Db 549 ovalAspIlyCysLeuSer---AsnProCys 558

RESULT 15

US-09-822-682-2
Sequence 2, Application US/09822682
Patent No. US20020119921A1

GENERAL INFORMATION:

APPLICANT: Detmar, Michael J.

TITLE OF INVENTION: THROMBOSPONDIN-2 AND USES THEREOF

FILE REFERENCE: 10287-051002

CURRENT APPLICATION NUMBER: US/09/822,682

PRIORITY FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/536,087

PRIORITY FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: 60/127,221

PRIORITY FILING DATE: 1999-03-31

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1172

TYPE: PRN

ORGANISM: Homo sapiens

US-09-822-682-2

Alignment Scores:

Pred. No.:	4.25	Length:	1172
Score:	95.50	Matches:	50
Percent Similarity:	35.55%	Conservative:	25
Best Local Similarity:	23.70%	Mismatches:	66
Query Match:	8.20%	Indels:	71
DB:	10	Gaps:	13

US-09-809-545a-1_COPY_535_1143 (1-609) x US-09-822-682-2 (1-1172)

QY 12 AAGGCGGTGACCCCTACACCAATGCTGGAATTAATTCAGTTGTGGCGGCTCTA 71
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QY 72 CAGCCCGGACT-----TGTCCAGGCCAACAGAGGAT-----TCTATGACAG 91
Db 402 GlnuIlyrprserProtrpalaGluTrpThrcIncysserValThrcysglYserGlyThr 421
QY 92 GCACGGTGTGT-----TGTCCAGGCCAACAGAGGAT-----TCTATGACAG 127
Db 422 ThrArgAlacysSerLeuSerLysCysAspThrArgIleArgGlnAspGlyYTrpSer 441
QY 128 -----CTTCATGTCACAGTGGCCCGGACCTGTCACAGTTCATGTCAT 160
Db 442 HistPrserProtrpserSerCysSerValThrcysglYalGlyAsnIle-ThrArgIl 461
QY 161 ATACTTGCATAGCTGCTT---TCCATATCCGCGCCGACCTGTCACAGTTCATGTCAT 217
Db 461 eArgLeucYsaSnsrProvalProGlnMeIglYlYsaSncys----- 476
QY 218 GAGGGCTCACCTTCGAGGCCGTGTGCGACCGGTGTACACACCTTCAGAGCTGC--GG 274
Db 477 -LysGlySerGly-----ArgGlnuThrLysAlacysGlnG 488
QY 275 CGCCCCCAACCCCAATCCCGGCTATGGCGGAGTAGTATCAAGAAGCAGTGTATGCA 334
Db 488 yAlaProCysProIleAspIlyArgTrp-----SerProtrp-- 500
QY 335 ATAAATTGTCACAGGTGTTAGCGATACCGCTACGCCACCCACCCCTGCCACTG 394
Db 501 -----SerProtrpserAlacysThVal-----Th 509
QY 395 CTGCTGCTACAGTACGAGAGTATTAGTGTGCGACCCCTACACACACAC-- 452
Db 509 rcysAlaGlylYleArgIleArgGlnuArgThrArgValCysAsnsrProGlnuProGlnuYrgl 529
QY 453 -----ACTTGC---TCCAGCCCCCAGCTACGGCGGTGGCGCATATGCTTTTGGCG 502
Db 529 yGlyLysAlacysValGlyAspValGlnuArgGlnMeCysAsnLysArgSerCysPr 549

Qy 503 CCTGACCGATGCCAAGACTAGAGCATGC 533
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Db 549 ovalaspGlyCysLeuSer---AsnProCys 558

Search completed: September 25, 2003, 12:06:50
Job time : 284.5 secs

QY	1	ATGACATAATAAAGGCCGTGAACCCCTACACCAATGGCTGAAATTAAATCCAGTTGTG	60
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QY	61	GGCGCGCTACAGACCCCGACTTCTATGACAGGACGCTGTGTGTGCCAGCCAAACAG	120
Db	1632	GGTCAGACTACAGCCCGGAATTCATACAGGACGCTCTGTGTGCCAGCCAAACAG	169
QY	121	GAGGGAATCTCCATATGTACAGTGGCCCCAGTTCACTTGATATATACCTTTCGAATTCGCTGGC	180
Db	1692	GAGGGAATCTCCATATGTACAGTGGCCCCAGTTCACTTGATATATACCTTTCGAATTCGCAAGGC	175
QY	181	TTTTCATATCCGGCGCCGACACTGCTGCACACTGCATATCCAGGGGGCTCACCTTGGAGGCGCT	240
Db	1752	TTCCCGTATCCAGCAGCCACCGCCGCGGCCCTTACCGAGGGCGCACCCTGGGAGGCCGC	181
QY	241	GGTGCAACCGTGTACACACACCTTCAGAGACTCGGGGCCCCCAACCCCAATTCGCCGACTAT	300
Db	1812	GGTGCAACCGTGTACACACACCTTCAGAGGCCCGGGGCCCCCGCCCGATCCCGGCGTAC	187
QY	301	GGCGGAGTAGTGTATCAAGAGCCACAGTATGGCAATAATTGCTACAGGGTGTATACGT	360
Db	1872	GGCGGAGTAGTGTATAC - - CAGGATGGATTTTATGGTGACACATTTAATGCTGTATGCT	1928

Oy	361	GCATACCGCCTACGGCCACCCACCCCTGCACACTGGTGGCTACAGTA-----	410
Dp	1930	GCATACCGCCTACGGCCACCCCTACCCCTGCACACTGGCCTACAGTACAGAAATACG	19839
Oy	411	-----CAGTTACGACAGATT	427
Dp	1990	TTGCTCTTTCGTTGACGAGATGAATTTCTTGTAAACACTCTCGAGTTACGACAGATT	2049
Oy	428	ATGCTGCGGACCCCTACCCACACACACTTGGCTCCAGCCCCACCTACGGCGTTGGTGCA	487
Dp	2050	ATGCTGCGGACCCCTACCCACACAGACTTGGTCCAGCCCCACCTACGGCGTTGGTGCA	2109
Oy	488	TGAATGCTTTGGCGCCTTGAACCGATGCGAAGACTAGAGCCATGCTGATATGTGGTC	547
Dp	2110	TGAATGCTTTGGACCTTTGACTGATGTGCAGACACTAGAGGCACTGATATGTGGGCTC	2169
Oy	548	TGCTTTCTTTCTTCAATTCGAGCGCTAGTATATACCAAGGGGATACCAACGTTTGCCTCAT	607
Dp	2170	TCGTTCTTTCTTCAATTCGAGCGCTAGTATATACCGAGGGGATACCAACGTTTGGCTCAT	2229
Oy	608	A 608	
Dp	2230	A 2230	

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1      RESULT 2
2      US-09-176-657-5
3      ; Sequence 5, Application US/09176657
4      ; Patent No. 6020164
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Bandman, Olga
7      ; APPLICANT: Tang, Y. Tom
8      ; APPLICANT: Corley, Neil C.
9      ; APPLICANT: Guegler, Karl J.
10     ; APPLICANT: Lu, Aina
11     ; APPLICANT: Baughn, Mariah R.
12     ; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
13     ; FILE REFERENCE: PF-0611 US
14     ; CURRENT APPLICATION NUMBER: US/09/176,657
15     ; CURRENT FILING DATE: 1998-10-21
16     ; NUMBER OF SEQ ID NOS: 9
17     ; SOFTWARE: PERL Program
18     ; SEQ ID NO 5
19     ; LENGTH: 1506
20     ; TYPE: DNA
21     ; ORGANISM: Homo sapiens
22     ; FEATURE: _
23     ; OTHER INFORMATION: 1250374
24     -09-176-657-5

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Query Match	10.4%	Score	63.2	DB	3	Length	1506
Best Local Similarity	54.5%	Pred. No.	1e-09				
Matches	279	Conservative	0	Mismatches	193	Indels	40
						Gaps	6

[illegible]

Db	1008	CATTGAGGGGACAGGGGCGGACAGTAATATGTTGGAGTCCGCA-----GGGATACCTGCACAA	1064
OY	286	CCATTCGCCGGCCTATGCGGGAGTAGTATCAAGACCGCAGTGTATGGCAATAAATTGCTA	345
Db	1065	GCCTATCCCCCTCTATCCAGGGGTGGATATGACGCTCAAGATATGCAACAGCGCTCTACTTG	1124
OY	346	CAGAGTGGTTCAGCTGCATCCGCTACGCCGACGCCACCCCTGGCCACTGCTGTGCTTAC	405
Db	1125	CAC-----GGACGCCACCGCTGCTGGAGCGCGCTGCAGCCGCTTAC	1165
OY	406	AGTACACAGTACGGACAGATTATGCTGCGGACCCCTACACACACACTGCTTCAGCC	465
Db	1166	AGTACAGGTTATGGCAGGGGTGTACACAGCCACACCCCT---ACCATGCCCTTGCCCGCTGCC	1222
OY	466	CCGACCTACGGGCTGGTGGTCCATGATGCTTT	497
Db	1223	GCTAGCTATGAGATTGGCGCTGTGGCCAGTTT	1254

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RESULT 3
US-09-421-299-5
: Sequence 5, Application US/09421299
: Patent No. 6524579
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Aina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/09/421,299
: CURRENT FILING DATE: 1999-10-20
: EARLIER APPLICATION NUMBER: 09/176,657
: EARLIER FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: _
: OTHER INFORMATION: 1250374
US-09-421-299-5

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Query Match	10.4%	Score	63.2	DB	4	Length	1506
Best Local Similarity	54.5%	Pred. No.	1e-09				
Matches 279; Conservative	0	Mismatches	193	Indels	40	Gaps	6

OY	1	ATGCTATATAAAGGCGCGTAAACCCCTACACCACTGGCTGAAATTAATCACTTTG	60
Db	768	ATGACCAATATAGAAGATGTGCACACCAATATGCMAATGGTTGGAAATTAAAGCCAGTA	827
OY	61	GGCGGGCTTACAGCCCCGACTTCTATGACGAGCAAGGTGCT-----TGTGCCAG	111
Db	828	GGACTGTATATGTGTCCGAGTTATATGCACCACTTCAGCTTTCAAGCAGATGTGCC	887
OY	112	GCACAACGAGAGGGATCTTCATCATGTACAGTGGCCCACTTCATCTGTATATCTGTCA	171
Db	888	GGCAATGATGAGAGATGCCCTCTATACAGGAAGAGGGGTATCAACACTTACATTCCTTA	947
OY	172	----ATGCCGTGCTTCCATA---TCGGCGCCCACTGCTGCAGCTGCATACCGAGGGCT	225
Db	948	ATCTTCTCTGCTTCCCTTACCCCTACATGCACACCAACGAGCGGCTTTGAGAGGACC	1007
OY	226	CACCTTGAAGCCCTGTGTCGACAGCTGTACAACACTTCAGAGCTGGCGGCCCCCAACC	285
Db	1008	CATTGAGGGGCAAGGGCGGACAGTATATGTGTGCAGTCCGA---GGGTACTCTCCAA	1066
OY	286	CCAATCCCGGCTTATGGCGAGTGTGTATTAACAGCCAGTGTATGGCAATTAATTTGTA	345
Db	1065	GCATTCGCCCGCTATCCAGGGGTGGATATGAGGCTCATAGATATGACATAGCGCTACTGT	1124

[illegible]

RESULT 4

? Sequence 14, Application US/08232463
 ? Patent No. 5670367
 ? GENERAL INFORMATION:
 ? APPLICANT: DORNER, F.
 ? APPLICANT: SCHEIFLINGER, F.
 ? APPLICANT: FALKNER, F. G.
 ? TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ? NUMBER OF SEQUENCES: 52
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Foley & Lardner
 ? STREET: 1800 Diagonal Road, Suite 500
 ? CITY: Alexandria
 ? STATE: VA
 ? COUNTRY: USA
 ? ZIP: 22313-0299
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/232,463
 ? FILING DATE:
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US/07/935,313
 ? FILING DATE:
 ? APPLICATION NUMBER: EP 91 114 300.6
 ? FILING DATE: 26-AUG-1991
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BENT, Stephen A.
 ? REGISTRATION NUMBER: 29,768
 ? REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (703)836-9300
 ? TELEFAX: (703)683-4109
 ? TELEX: 899149
 ? INFORMATION FOR SEQ ID NO: 14:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 7218 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? IMMEDIATE SOURCE:
 ? CLONE: pTZgpt-F15
 ? US-08-232-463-14

Query Match	6.18;	Score 37.4;	DB 1;	length 7218;
Best Local Similarity	2.98;	Pred. No. 0.18;		
Matches	11;	Conservative 209;	Mismatches 165;	Indels 0;
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Db 1112 YY 1172

QY 241 GGTCGCACCGGTACACACCTTCAGACCTCGCGGCCCCACCCCCCAATCCGGCCTAT 300

Db 1172 YY 1233

QY 301 GCGGAGTAGTGTATCAAGAGCCAGGTATGGCATAAATTGCTACAGGGTGTACGCT 360

Db 1232 YY 1291

QY 361 GCATACCGCTACGGCCACGCCACCCCTGCCACTGCTGCTGCTACAGTGACAGTACGGA 420

Db 1292 YY 1351

QY 421 CGAGTTATGCTGCGACCCCTACACACACACACTTGTCCAGCCCCACCTACGGCGCTT 480

Db 1352 YY 1411

QY 481 GGTGCATGAAATGCTTTGGCGCCCT 505

Db 1412 YYYYYYYYYYYYYYYYYYYYYYYYGT 1436

RESULT 5

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US-09-103-840A-1/C
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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Best Local Similarity	51.58;	Pred. No. 4.3;		
Matches	85;	Conservative	0;	Mismatches 80;
			Indels	0;
			Gaps	0;

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OY	418	GGAGGAGTTTATGCTGGCGGACCCCTTACCACACACACTTGTCCAGCCCCACCTACGGC	477
Db	39444416	GGCGGCACCGCCGGGTGGCGCGCGGCGCGCGGACCTCGCCGCTTCGGCGCGCGGATACGGCC	3944357
OY	478	GTTGGTGCAATGAATGCTTTTGGCCCTTCAGCCATGGCAAGACT	522
Db	39444356	GTTGCGCGCGCTTGGCGCGCATATGCCGCCACATGTCGCGCGCCGACAGGCT	39444312

RESULT 6

US-08-323-442B-1
: Sequence 1, Application US/08323433
: Patent No. 5654170
: GENERAL INFORMATION:
: APPLICANT: KLINER, KATHERINE W.
: APPLICANT: LANDES, GREGORY M.
: APPLICANT: BURN, TIMOTHY C.
: APPLICANT: CONNORS, TIMOTHY D.
: APPLICANT: DACKOWSKI, WILLIAM R.

```

1 APPLICANT: GERMINO, GREGORY
2 APPLICANT: QIAN, FENG
3 TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
4 NUMBER OF SEQUENCES: 8
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Darby & Darby PC
7 STREET: 805 Third Avenue
8 CITY: New York
9 STATE: NY
10 COUNTRY: USA
11 ZIP: 10022
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOSS
16 SOFTWARE: Patent Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/323,443B
19 FILING DATE: 12-OCT-1994
20 CLASSIFICATION: 435
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Ludwig, S. Peterer
23 REGISTRATION NUMBER: 25,351
24 REFERENCE/DOCKET NUMBER: 0372/0A462
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (212) 527-7700
27 TELEFAX: (212) 753-6237
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 31571 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: DNA (genomic)
35 HYPOTHEITICAL: NO
36 ORIGINAL SOURCE:
37 ORGANISM: Homo sapiens
38 IMMEDIATE SOURCE:
39 CLONE: PRDI GENOMIC
40 US-08-323-443B-1
41
42 Query Match          6.0%; Score 36.8; DB 1; Length 31571;
43 Best Local Similarity 47.3%; Pred.No. 0.54;
44 Matches   95; Conservative    0; Mismatches 106; Indels     0; Gaps      0;
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50 Oy       112 GCCAACACAGAGAGATTTCCATTGACAGTGGGCCCATGTTCACTTGATATATCTTGCA 171
51         ||| | | | | | | | | | | | | | | | | | | | | | | | | |
52 Db       25487 GCCAAGNNTNGGGGNGNTGGACAAGAAAGTGGGCCCTGAAGTCTGTTTTCCGCCCTCCC 25548
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54 Oy       172 ATGCGCTGGCTTTCCATATCCGCGCCGCACATGCTGCACAGTCGATACCAGAGGGGCTCAC 231
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56 Db       25547 GGCGCTGGCTCTTGCTCTCTGCTGCGCCGAGTGACAGCTGACACTTGAGAGGCGGTGCC 25608
57               ||||||| | | | | | | | | | | | | | | | | | | | | |
58 Oy       232 CGAAGCGCGTGTGGACACCCTG 252
59         | | | | | | | | | | | | | | | | | | | | | | | | | |
60 Db       25607 CTGCGCACGACGCCCTCAGTG 25627
61               | | | | | | | | | | | | | | | | | | | | | | | |
62
63 RESULT 7
64 US-09-103-840A-2
65 Sequence 2, Application US/09103840A
66 Patent No. 6294328
67 GENERAL INFORMATION:
68 APPLICANT: FLEISCHMAN, Robert D.
69 APPLICANT: WHITE, Owen R.
70 APPLICANT: FRASER, Claire M.
71 APPLICANT: VENTER, John C.
72 TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
73 TUBERCULOSIS

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[illegible]


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? TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
? TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
? NUMBER OF SEQUENCES: 6
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
? STREET: 1 Becton Drive
? CITY: Franklin Lakes
? STATE: NJ
? COUNTRY: US
? ZIP: 07417
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/402,282
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Fugit, Donna R.
? REGISTRATION NUMBER: 32,135
? REFERENCE/DOCKET NUMBER: P-3283
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15664 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 222..425
? OTHER INFORMATION: /function= "potential open reading
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? NAME/KEY: misc_feature
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? LOCATION: 8033..8236
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? LOCATION: 8244..9443
? OTHER INFORMATION: /function= "potential open reading
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? OTHER INFORMATION: /function= "potential open reading
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;   TOPOLOGY: linear
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;   MOLECULE TYPE: DNA (genomic)

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NAME/KEY: misc_feature
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LOCATION: 15429..15664
OTHER INFORMATION: /function="potential open reading
OTHER INFORMATION: frame"
-08-508-004-3

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Best Local Similarity 47.8%; Pred. No. 2.5;
Matches 99; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 220 GGGGCTACCTTCGAGCGCGGTGTCGACCGCTGTACAACTTTCAGAGCTCGGGCCCC 279
DB 720 GGGGCTACCTTCGAGCGCGGTGTCGACCGCTGTACAACTTTCAGAGCTCGGGCCCC 279
QY 280 CCACCCCAATCCCGCTATGCGAGTAGTGTATCAAGACCAAGTATGCAATATAA 339
DB 780 GCGCTCGCTATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 839
QY 340 TTGCTACAGGGGTGTACGCTGCATACGCTACGCCAGCCAGCCCTGCGCACTGCT 399
DB 840 CTGTACTTGTCTCGCGAGCGCGGTTCGCTATGACAGCGCGCGCGCGCGCGCGCGCA 899
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DB 900 GGCACACCGCTGTGCGCAGCGCGCAT 926

RESULT 14
US-08-402-066-3

Sequence 3, Application US/08402066
Patent No. 5612182
GENERAL INFORMATION:
APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,066
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3283
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 222..425
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NAME/KEY: misc_feature
LOCATION: 14771..15154
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OTHER INFORMATION: //function= "potential open reading
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15429..15664
OTHER INFORMATION: //function= "potential open reading
OTHER INFORMATION: frame"
US-08-402-066-3

Query Match          5.6%; Score 34.2; DB 1; Length 15664;
Best Local Similarity 47.8%; Pred. No. 2.5;
Matches   99; Conservative    0; Mismatches 108; Indels     0; Gaps      0;

QY      220 GGGGCTCAACCTTCAGAGCGGTGTTGCACCCTGTATCACAACACTTATAGAGCTCCGCCGCC 279
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QY      720 GGGCTGTACTGAGGAGGGCGGTGTGTCGAATGATCCGCGAAGAATGCATATCGGTGGCC 779
Db       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      280 CCACCCCCCATCCGCGCTATTGCGGAGTAGTGTAATGAAGCACAGTATGGCAAATAAA 339
Db       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      780 GCCGTGCGTATCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 839
Db       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      340 TTGCTACAGGTTGTTACGCTGCATACCCTACGCCCCAGCCCACCCCTGCCACTGCTGCT 399
Db       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      840 CTGTACTTGTCGGCGAGCGCGGGGTTCGGCTATGAGAGCGCGCGCGGTGTATCTGCCGA 899
Db       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      400 GCCTACAGTAGACAGTTACGAGAGATT 426
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QY      900 GGCCACACCGTGTGCCAACGCCGCGAT 926
Db       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
US-08-402-068-3
Sequence 3, Application US/08402068
Patent No. 5633159
GENERAL INFORMATION:
APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Bayer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,068
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugitt, Donna R. 32,135
REGISTRATION NUMBER: P-3283
REFERENCE/DOCKET NUMBER: 3;
SEQUENCE CHARACTERISTICS:
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QY	280	99	5.6%	339	15664
DB	780	99	47.8%	839	2.5
QY	340	99	5.6%	399	15664
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Thu Sep 25 13:04:40 2003

us-09-809-545a-1_copy_535_1143.rni

Page 11

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Search completed: September 25, 2003, 11:56:31
Job time : 76 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:39:29 ; Search time 172 Seconds
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Title: US-09-809-545a-1_COPY_535_1143

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	609	100.0	1340	10	US-09-809-545A-1
2	428.6	70.4	2372	9	US-09-794-591-1
3	79.4	13.0	1843	11	US-09-919-031-1
4	63.2	10.4	1506	12	US-10-359-385-5
5	55.2	9.1	60	12	US-09-908-975-7420
6	36.8	6.0	1049	12	US-10-140-472-358
7	36.8	6.0	1049	12	US-10-141-761-358
8	36.8	6.0	1049	12	US-10-142-885-358
9	36.8	6.0	1049	14	US-10-123-155-358
10	36.8	6.0	1049	14	US-10-146-731-358
11	35.6	5.8	2538	15	US-10-156-761-4134
12	35.6	5.8	9025608	14	US-10-156-761-1
13	35.4	5.8	4400	14	US-10-184-644-202
14	35.4	5.8	440	14	US-10-184-634-202
15	35.4	5.8	660	14	US-10-144-929-48
16	34.4	5.6	1209	12	US-10-101-510-143

C 17	34.2	5.6	594	12	US-10-140-472-10	Sequence 10, Appl
C 18	34.2	5.6	594	12	US-10-141-761-10	Sequence 10, Appl
C 19	34.2	5.6	594	12	US-10-142-885-10	Sequence 10, Appl
C 20	34.2	5.6	594	14	US-10-123-155-10	Sequence 10, Appl
C 21	34.2	5.6	594	15	US-10-146-731-10	Sequence 88, Appl
C 22	34	5.6	735	14	US-10-184-644-88	Sequence 88, Appl
C 23	34	5.6	735	14	US-10-184-644-88	Sequence 88, Appl
C 24	33.4	5.5	538	12	US-10-084-843-180	Sequence 180, Appl
C 25	33.4	5.5	538	12	US-10-084-843-180	Sequence 175, Appl
C 26	32.8	5.4	535	12	US-10-084-843-175	Sequence 175, Appl
C 27	32.8	5.4	535	12	US-10-193-002-166	Sequence 166, Appl
C 28	32.8	5.4	786	14	US-10-156-761-6751	Sequence 6751, Ap
C 29	32.8	5.4	3063	13	US-10-027-632-114387	Sequence 114387,
C 30	32.8	5.4	3063	13	US-10-027-632-114388	Sequence 114389,
C 31	32.8	5.4	3063	13	US-10-027-632-114389	Sequence 127378,
C 32	32.6	5.4	815	13	US-10-027-632-127378	Sequence 649, App
C 33	32.6	5.4	45191	15	US-10-080-170-649	Sequence 402, App
C 34	32.2	5.3	653	14	US-10-184-644-402	Sequence 402, App
C 35	32.2	5.3	653	14	US-10-184-634-402	Sequence 3417, Ap
C 36	32.2	5.3	951	10	US-09-738-626-3417	Sequence 180, App
C 37	32.2	5.3	1071	11	US-09-880-505-180	Sequence 24, Appl
C 38	32.2	5.3	1071	12	US-10-205-979-24	Sequence 180, App
C 39	32.2	5.3	1071	13	US-10-051-643-180	Sequence 180, App
C 40	32.2	5.3	1185	10	US-09-738-626-3418	Sequence 3418, Ap
C 41	32.2	5.3	3309400	10	US-09-738-626-1	Sequence 1, Appl
C 42	32	5.3	696	12	US-10-140-472-354	Sequence 354, App
C 43	32	5.3	696	12	US-10-141-761-354	Sequence 354, App
C 44	32	5.3	696	12	US-10-142-885-354	Sequence 354, App
C 45	32	5.3	696	14	US-10-123-155-354	Sequence 354, App

ALIGNMENTS

RESULT 1
US-09-809-545A-1
; Sequence 1, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-809-545A-1

Query Match 100.0%; Score 609; DB 10; Length 1340;
Best Local Similarity 100.0%; Pred. No. 3.9e+195;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGACTAATAAAGGCCGCTGAAACCCCTACCAATGCTGGAAATTAATCACTGTCG	60
DB	535	ATGACTAATAAAGGCCGCTGAAACCCCTACCAATGCTGGAAATTAATCACTGTCG	594
QY	61	GGCGCGGTACAGCCGCTGATGAGGAGGAGGCTGTGTGCCAGGCAACAG	120
DB	595	GGCGCGGTACAGCCGCTGATGAGGAGGAGGCTGTGTGTGCCAGGCAACAG	654
QY	121	GAGGAGTCTTCATGATGAGTGGCCGCTGCTGTATATATCTTGCATGCTGGC	180
DB	655	GAGGAGTCTTCATGATGAGTGGCCGCTGCTGTATATATCTTGCATGCTGGC	714
QY	181	TTTTCATATCCGCGCCGCTGCTGAGTGCATACGAGGGGCTACCTGAGGCGCT	240
DB	715	TTTTCATATCCGCGCCGCTGCTGAGTGCATACGAGGGGCTACCTGAGGCGCT	774

QY	241	GGTGGCAACCGGTTCACACACCTTCAAGAGCTGGGGGCCCCACCCCAATCCGGGCTAT	300
Db	775	GGTGGCAACCGGTTCACACACCTTCAAGAGCTGGGGGCCCCACCCCAATCCGGGCTAT	834
QY	301	GGCGAGTATAGTATCTCAAGAAGCCAGTGTATGGCATATAATTGCTCAAGAGGTGGTTACGCT	360
Db	835	GGCGAGTATAGTATCTCAAGAAGCCAGTGTATGGCATATAATTGCTCAAGAGGTGGTTACGCT	894
QY	361	GCATACCGCTACGCGCCAGCCCAACCCCTGGCCACTGCTGGCTACAGTACAGTTACGGA	420
Db	895	GCATACCGCTACGCGCCAGCCCAACCCCTGGCCACTGCTGGCTACAGTACAGTTACGGA	954
QY	421	CGAATTATATGCTGGCCGACACCCTTACCACACACACTTGTCCAGCCGCCCACTAAGGCGTT	480
Db	955	CGAATTATATGCTGGCCGACACCCTTACCACACACACTTGTCCAGCCGCCCACTAAGGCGTT	1014
QY	481	GGTGCATATGAATGCTTTTGGCGCCCTTGGACCATGCCAAGACTTAGAGGACATGCTGATGAT	540
Db	1015	GGTGCATATGAATGCTTTTGGCGCCCTTGGACCATGCCAAGACTTAGAGGACATGCTGATGAT	1074
QY	541	GTGGGTCCTCGTCTTCTTCTCATTTGSCAGGCTATATATACCAAGGGGGATACCAACCGTTTT	600
Db	1075	GTGGGTCCTCGTCTTCTTCTCATTTGSCAGGCTATATATACCAAGGGGGATACCAACCGTTTT	1134
QY	601	GCTTCATAT 609	
Db	1135	GCTTCATAT 1143	

RESULT 2
US-09-794-591-1

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: Sequence 1 Application US/09794591
: Patent No. US20010018198A1
:
: GENERAL INFORMATION:
: APPLICANT: Pulst, Stefan M.
: APPLICANT: Shibata, Hiroki
: TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
: TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
: FILE REFERENCE: CE 3093
: CURRENT APPLICATION NUMBER: US/09/794,591
: CURRENT FILING DATE: 2001-02-26
: PRIOR APPLICATION NUMBER: 09/145,391
: PRIOR FILING DATE: 1998-09-01
: NUMBER OF SEQ. ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2372
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (987)..(1979)
: OS-09-794-591-1

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Best Local Similarity	82.0%	Pred. No. 4.5e-134		
Matches 542	Conservative 0	Mismatches 64	Indels 55	Gaps 2

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RESULT 3

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US-09-919-039-266
Sequence 266, Application US/09919039
Publication NO. US20030108871A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 266
LENGTH: 1843
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
NAME/KEY: unsure
LOCATION: 1824
OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

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Query Match	13.0%	Score 79.4	DB 11	Length 1843
Best Local Similarity	68.3%	Pred. No. 4.2e-16		
Matches 110; Conservative	0	Mismatches 51	Indels 0	Gaps 0

QY	166	TCTTCGAAATGCTCTGCTTCCATATCCGGGCCCCCACTCTGACACTGCATACCGAGGGGCT	225
	1312	TATCCAGTGAAGGGGGTTCCCTTACCACCAACCGGCGACAGCGCTTGCCTTACCGAGGGGCGCA	1371
Db			
QY	226	CACCTTCGAGGCGCGTGTGCGCACCGCTGTACAAACCTTCAGAGCTGCGCGGCCCCCAACC	285
	1372	CATCTTCGGGGGCCGGGGCCGGGCGGTATATATATCATTTTGGGCTGGGCCACCCCCCAACC	1431
Db			

OY 286 CCAATCCCGCCTATGCGGAGTAGTGTATCAAGCCAGT 326
DB 1432 CCCATCCCGCCTATGCGGAGGAGGAGTGTATCAAGCCAGT 1472

RESULT 4

US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: 1250374
US-10-359-385-5

Query Match 10.4%; Score 63.2; DB 12; Length 1506;
Best Local Similarity 54.5%; Pred. No. 1.2e-10;
Matches 279; Conservative 0; Mismatches 193; Indels 40; Gaps 6;

OY 1 ATGACTAATATAAAGCCGTGAACCCCTACACCAATGCTGGAAATTAATCACTGTTG 60
DB 768 ATGACCAATATAAAGAGTGTACACCATATGCAAAATGTTGAAATTAAGCCAGT 827
OY 61 GCGGGGTGTACAGCCCGACCTTCTTATGAGGACGCGTCTGT-----TGTCGAG 111
DB 828 GGAGCTGTATGATGTCGAGATATATGAGCATCGCTTCAAGCAGATGTGCTTA 887
OY 112 GCCAACGAGGAGGATCTTCATGATGAGTGGCCCGACCTTCTATATCTGTGTA 171
DB 888 GGCAATGATGAGAGTGGCCCTATACAGAAAGGGGGTATCAACACTTACATTCCTTA 947
OY 172 ---ATGCTGCTTTCATATA---TCCGGCCGACCTGCTGACAGTGCATACCGAGGGCT 225
DB 948 ATCATTCCTGCGTTCCTTACCTACTGACGACACGACGCGCTTTCAGAGGAGCC 1007
OY 226 CACCTTCGAGGCGGTGTGACACCGTGTACAAACCTTACAGAGTGGCGGCCGCCACC 285
DB 1008 CATTTGAGGGGAGAGGGGCGAGATATGTGTGACGTCGA---GCGGTACTCTCACA 1064
OY 286 CCAATCCCGCCTATGCGGAGTAGTGTATCAAGAGCGTATGCAATAAATTGCTA 345
DB 1065 GGCATCCCGCCTATTCAGAGGGTGTATGACAGCTTACAGATATGACAGCGCTACTG 1124
OY 346 CAGGTGTGTACGTCATACCGTACAGCCGACCCCTGACCACTGCTGCTGCTAC 405
DB 1125 CAAC-----CGAGCGACCGGTGCTGACGCGCGCTTACCGCGCTTAC 1165
OY 406 AGTGACAGTATACGAGAGTATAGTCCGACCCCTACACACACACTTCTCCAGCC 465
DB 1166 AGTGACAGTATAGGAGGAGTGTACACAGCGACCCCT---ACCATGCGCTTCCCTGCC 1222
OY 466 CCCACCTACGCGGCTGTGTGTCGATGATGCTT 497
DB 1223 GCTACGATGAGAGTGGCGCTGTGGCGAGTTT 1254

RESULT 5
US-09-908-975-7420
; Sequence 7420, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSEMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Ilat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7420
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-7420

Query Match 9.1%; Score 55.2; DB 12; Length 60;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 57; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 499 GCGCCCTGACCGATGCAAGACTAGACCATGCTGATGATGTGGTCTGCTTCT 558
DB 1 GCACCTTACTGATGATGCAAGACTAGACCATGCTGATGATGTGGTCTGCTTCT 60

RESULT 6
US-10-140-472-358/c
; Sequence 358, Application US/10140472
; Publication No. US20030138888A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: US/10/140,472
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 2002-05-06
; NUMBER OF SEQ ID NOS: 550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-472-358

Query Match 6.0%; Score 36.8; DB 12; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.083;

Matches	27	Conservative	167	Mismatches	326	Indels	2	Gaps	1
OY	7	AAAAAAAAAGCGCGTGAACCCCTTACACCAATGGCTGGAAATTAATCCAGTTGTGGCGCG	66						
Db	905	ABT..HHMHRB..TTRGGH.S..Y..RCM..MTMG..DR..KMBHW..R..DSTAKBRK...SBS..S	846						
OY	67	GTCACAGACCCCGCACTTCTATGACAGGACGCGTGTGTGTGCCAGGCCAACACGAGAGCGA	126						
Db	845	S...NA.H..GAR.H.S.BS.CMDTC.CGABHAT..R..AB.ADNBMWB..WBTMGAG..	786						
OY	127	TCTTCATGTACAGTGGGCCCAAGTTCACTTGTATATACTTGTGCATATGCTGGCTTCC	186						
Db	785	..YND..KM..BN..SAM..K..MNSS.H..RY...TH...RMA..SY..NM..	726						
OY	187	TATCGGCGCGCACTGCTGTCAGCTGCAATACGAGAGGCGTACACTTCGAGCGCGTGTGCG	246						
Db	725	..SYGNS.Y..BAA..NDS.H.A..NM.G..MMS.SM.CMWT..S.NM.N..KCH.BCS..	666						
OY	247	ACCGTGTACACACACCTTTCAGAGCTGGCGGCGCCCGCCACCCCAATCCGCGCTAATGGCGGA	306						
Db	665	..S..SNMS.H...M..NM...RYNHC..YW..BH.DNCY...A-Y..S.S.KAYSASS..	608						
OY	307	GTAAGTATACAGAGCCAGCTGTATGGCAATTAATTGCTACAGAGGTGTAGCTGCATAC	366						
Db	607	HHNKK..M..BM.NMA.N.KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H	548						
OY	367	CGCTACGCGCCAGCCACCCCTGCGCAGCTGCTGCTGCTACGTGACAGTACGAGAGTT	426						
Db	547	..RY..T...SCN.A.S..NCS.N.GM..S.D..HSEMB...SNMS.H.A.CMRGS.N	488						
OY	427	TATCGTGGCAGCCCTTACACACACACTTCTCCAGCGCCCGCTACGAGCGGTGTGCC	486						
Db	487	BSK..ST..NM..YGSYTRMHR..RD...B...RS.BSYATNSG..CB..SHCS.S.MBS..	428						
OY	487	ATGAATGCTTTTGGCGCCCTTGACCGATGCCAAGACTAGAGAC	528						
Db	427	H.BM..YM..M.KS..NT..M..NAC.H.B..N..ND..S.N.SM	386						
RESULT 7									
US-10-141-761-358/c									
: Sequence 358, Application US/10141761									
: Publication No. US20030148432A1									
: GENERAL INFORMATION:									
: APPLICANT: Baker, Kevin P.									
: APPLICANT: Beresini, Maureen									
: APPLICANT: DeForge, Laura									
: APPLICANT: Desnoyers, Luc									
: APPLICANT: Filvaroff, Ellen									
: APPLICANT: Gao, Wei-Qiang									
: APPLICANT: Gerritsen, Mary E.									
: APPLICANT: Goddard, Audrey									
: APPLICANT: Godowski, Paul J.									
: APPLICANT: Guirney, Austin L.									
: APPLICANT: Sherwood, Steven									
: APPLICANT: Smith, Victoria									
: APPLICANT: Stewart, Timothy A.									
: APPLICANT: Tumas, Daniel									
: APPLICANT: Watanabe, Colin K									
: APPLICANT: Wood, William									
: APPLICANT: Zhang, Zelin									
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC									
: FILE REFERENCE: P33081C198									
: CURRENT APPLICATION NUMBER: US/10/141,761									
: CURRENT FILING DATE: 2002-05-08									
: Prior Application removed - See Palm or File Wrapper									
: NUMBER OF SEQ ID NOS: 550									
: SEQ ID NO 358									
: LENGTH: 1049									
: TYPE: PRT									
: ORGANISM: Homo Sapien									
US-10-141-761-358									

[illegible]


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RESULT 13
US-10-184-644-202/c
; Sequence 202, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; PRIOR FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 202
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-202

Query Match
Best Local Similarity 15.9%; Score 35.4; DB 14; Length 440;
Matches 52; Conservative 88; Mismatches 188; Indels 0; Gaps 0;

OY 143 GCCCAGTTCACCTGTATATACCTTGCAATGCGCTTGCTTCATATCCGGCCGACCTG 202
DB 437 SST.HMN.THMN..C.MSM.NMW.AH.N.KC.SA.SMBANBCBTHCCSCSWSSC.CYRN 378
OY 203 CTCAGCTGCATACCGAGGGCTCACCCTTGAGAGCGCTGTGCTGCACCGCTAGACACCT 262
DB 377 HCSGC..YNC.MS..YKNSBC.CY.C..CS.CSCYT.NC.M.GC.MDCNCCSCDNC 318
OY 263 TCAGAGTGGCGGGCCCCCAATCCGGCTATGCGGAGTAGTATCAAGAGC 322
DB 317 SSCASSCWS.SCHYSCSNCSSCCSSCCSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 258
OY 323 CAGTGTATGCAATTAATGCTACAGGGTGTACGCTGATACCGCTAGCCGACCA 382
DB 257 SCSSCS.SCSGCCSSNSCCSSCS..NAGC.N.NSTYBSCRC..TBTC.AMAC.N..CCN 198
OY 383 CCCCTGCCACTGCTGCTGCTACAGTAGACAGTACGAGCAGTTATGCTGCGACCCCT 442
DB 197 CC.CW.TC..NKC.SCHSNC.RCDBW.AC.CC.NC.C.CC.CC.SC..CDCCSA.WTCS 138
OY 443 ACCACACACACTGCTCTCCAGCCGCCAC 470
DB 137 C.BC.MSCYBTHTCDY.BH.T.YC..DC 110

RESULT 14
US-10-184-634-202/c
; Sequence 202, Application US/10184634
; Publication No. US2003006864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
```

```
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; PRIOR FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 202
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-202

Query Match
Best Local Similarity 15.9%; Score 35.4; DB 14; Length 440;
Matches 52; Conservative 88; Mismatches 188; Indels 0; Gaps 0;

OY 143 GCCCAGTTCACCTGTATATACCTTGCAATGCGCTTGCTTCATATCCGGCCGACCTG 202
DB 437 SST.HMN.THMN..C.MSM.NMW.AH.N.KC.SA.SMBANBCBTHCCSCSWSSC.CYRN 378
OY 203 CTCAGCTGCATACCGAGGGCTCACCCTTGAGAGCGCTGTGCTGCACCGCTAGACACCT 262
DB 377 HCSGC..YNC.MS..YKNSBC.CY.C..CS.CSCYT.NC.M.GC.MDCNCCSCDNC 318
OY 263 TCAGAGTGGCGGGCCCCCAATCCGGCTATGCGGAGTAGTATCAAGAGC 322
DB 317 SSCASSCWS.SCHYSCSNCSSCCSSCCSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 258
OY 323 CAGTGTATGCAATTAATGCTACAGGGTGTACGCTGATACCGCTAGCCGACCA 382
DB 257 SCSSCS.SCSGCCSSNSCCSSCS..NAGC.N.NSTYBSCRC..TBTC.AMAC.N..CCN 198
OY 383 CCCCTGCCACTGCTGCTGCTACAGTAGACAGTACGAGCAGTTATGCTGCGACCCCT 442
DB 197 CC.CW.TC..NKC.SCHSNC.RCDBW.AC.CC.NC.C.CC.CC.SC..CDCCSA.WTCS 138
OY 443 ACCACACACACTGCTCTCCAGCCGCCAC 470
DB 137 C.BC.MSCYBTHTCDY.BH.T.YC..DC 110

RESULT 15
US-10-144-929-48
; Sequence 48, Application US/10144929
; Publication No. US20030069405A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2014P1
; CURRENT APPLICATION NUMBER: US/10/144,929
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: PCT/US98/17044
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (393)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (401)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-144-929-48
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Query Match	5.88;	Score 35.4;	DB 14;	Length 660;
Best Local Similarity	46.68;	Pred. No. 0.2;		
Matches 102; Conservative	3;	Mismatches 114;	Indels 0;	Gaps 0;

[illegible]

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search completed: September 25, 2003, 11:54:09
job time : 186 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:41:09 ; Search time 54 Seconds
(Without alignments)
4977.821 Million cell updates/sec

Title: US-09-809-545a-1_COPY_535_1143

Perfect score: 609

Sequence: 1 atgacataataaaagccgtf.....acacccgtttgtccatcat 609

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NH:*
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2: /cgn2_6/p10data/1/lna/5B.COMB.seq:*
3: /cgn2_6/p10data/1/lna/6A.COMB.seq:*
4: /cgn2_6/p10data/1/lna/6B.COMB.seq:*
5: /cgn2_6/p10data/1/lna/PC10S.COMB.seq:*
6: /cgn2_6/p10data/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	11.5	2372	3	US-09-145-391-1
2	18	3.0	615	3	US-09-286-284-29
3	18	3.0	664	3	US-09-286-284-28
4	18	3.0	3364	4	US-09-930-181-3
5	18	3.0	3431	4	US-09-632-098-1
6	18	3.0	3468	4	US-09-632-098-3
7	18	3.0	4830	3	US-09-286-284-7
8	17	2.8	36	4	US-09-337-307A-10
9	17	2.8	1757	1	US-08-199-779-2
10	17	2.8	1757	5	US-08-578-615A-105
11	17	2.8	1757	5	PCT-US94-07770-105
12	17	2.8	1812	1	US-08-199-779-1
13	17	2.8	1812	3	US-08-578-615A-104
14	17	2.8	1812	5	PCT-US94-07770-104
15	17	2.8	45546	4	US-09-146-053-6
16	17	2.8	536165	4	US-09-214-808-1
17	16	2.6	390	4	US-09-328-352-2282
18	16	2.6	429	4	US-09-252-991A-1762
19	16	2.6	437	1	US-08-631-200-3
20	16	2.6	437	1	US-08-631-200-4
21	16	2.6	437	1	US-08-631-200-5
22	16	2.6	437	1	US-08-829-553-3
23	16	2.6	437	1	US-08-829-553-4
24	16	2.6	437	1	US-08-829-553-5
25	16	2.6	437	2	US-08-922-267A-3
26	16	2.6	437	2	US-08-922-267A-4
27	16	2.6	437	2	US-08-922-267A-5

28	16	2.6	437	2	US-08-936-707A-3	Sequence 3, Appl1
29	16	2.6	437	2	US-08-936-707A-4	Sequence 4, Appl1
30	16	2.6	437	2	US-08-936-707A-5	Sequence 5, Appl1
31	16	2.6	437	2	US-08-936-706A-3	Sequence 3, Appl1
32	16	2.6	437	2	US-08-936-706A-4	Sequence 4, Appl1
33	16	2.6	437	2	US-08-936-706A-5	Sequence 5, Appl1
34	16	2.6	437	3	US-09-248-203-3	Sequence 3, Appl1
35	16	2.6	437	3	US-09-248-203-4	Sequence 4, Appl1
36	16	2.6	437	3	US-09-248-203-5	Sequence 5, Appl1
37	16	2.6	437	3	US-09-406-071-3	Sequence 3, Appl1
38	16	2.6	437	3	US-09-406-071-4	Sequence 4, Appl1
39	16	2.6	437	3	US-09-406-071-5	Sequence 5, Appl1
40	16	2.6	437	3	US-08-905-223-86	Sequence 86, Appl1
41	16	2.6	480	1	US-08-630-592-5	Sequence 5, Appl1
42	16	2.6	480	1	US-08-714-991-5	Sequence 5, Appl1
43	16	2.6	480	3	US-09-032-365A-5	Sequence 5, Appl1
44	16	2.6	833	2	US-08-837-029-1	Sequence 1, Appl1
45	16	2.6	918	4	US-09-107-532A-2095	Sequence 2095, Ap

ALIGNMENTS

```
RESULT 1
US-09-145-391-1
: Sequence 1, Application US/09145391
: Patent No. 6194171
: GENERAL INFORMATION:
: APPLICANT: Puist, Stefan M.
: APPLICANT: Shibata, Hiroki
: TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
: TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
: FILE REFERENCE: CE 3093
: CURRENT APPLICATION NUMBER: US/09/145.391
: CURRENT FILING DATE: 1998-09-01
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2372
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (987)..(1979)
US-09-145-391-1

Query Match      11.5%; Score 70; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 9.6e-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      511 GATGCCAAGACTGAGACCATGCGATGATGATGCGTCTGTTCTTCATTCAGACGCT 570
DB      2133 GATGCCAAGACTGAGACCATGCGATGATGATGATGCGTCTGTTCTTCATTCAGACGCT 2192
QY      571 AGTATATACC 580
DB      2193 AGTATATACC 2202

RESULT 2
US-09-296-284-29
: Sequence 29, Application US/09296284A
: Patent No. 6204040
: GENERAL INFORMATION:
: APPLICANT: Choi, Eun-Sung
: APPLICANT: Rhee, Sang-Ri
: APPLICANT: Lee, Eun-Hae
: TITLE OF INVENTION: Glucosyltransferase Suboxydase Sorbitol Dehydrogenase, Genes
: TITLE OF INVENTION: and Methods of Use Thereof
: FILE REFERENCE: 1533.0870000
: CURRENT APPLICATION NUMBER: US/09/296.284A
: CURRENT FILING DATE: 1999-04-22
: NUMBER OF SEQ ID NOS: 87
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SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-29

Query Match 3.0%; Score 18; DB 3; Length 615;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 GCGCCCCACCCCAATC 291
|||||
DB 48 GCGCCCCACCCCAATC 65

RESULT 3
US-09-296-284-28
; Sequence 28, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
; APPLICANT: Choi, Eun-Sung
; APPLICANT: Rhee, Sang-Ki

; TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
; FILE REFERENCE: 1533.0870000
; CURRENT APPLICATION NUMBER: US/09/296,284A
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-28

Query Match 3.0%; Score 18; DB 3; Length 664;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 GCGCCCCACCCCAATC 291
|||||
DB 97 GCGCCCCACCCCAATC 114

RESULT 4
US-09-930-181-3/C
; Sequence 3, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies

; TITLE OF INVENTION: Full-Length Serine Protein Kinase In Brain and Pancreas
; FILE REFERENCE: 160 101 VI
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3

Query Match 3.0%; Score 18; DB 4; Length 3364;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GCGGCGCCCAACCCCA 288
|||||

DB 3039 GCGGCGCCCAACCCCA 3022

RESULT 5
US-09-632-098-1
; Sequence 1, Application US/09632098
; Patent No. 6420154
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.

; APPLICANT: Balndur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3431
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)..(2442)
US-09-632-098-1

Query Match 3.0%; Score 18; DB 4; Length 3431;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GCGCCCAACCCCAATCC 293
|||||
DB 2978 GCGCCCAACCCCAATCC 2995

RESULT 6
US-09-632-098-3
; Sequence 3, Application US/09632098
; Patent No. 6420154
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.

; APPLICANT: Balndur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)..(2472)
US-09-632-098-3

Query Match 3.0%; Score 18; DB 4; Length 3468;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GCGCCCAACCCCAATCC 293
|||||
DB 3015 GCGCCCAACCCCAATCC 3032

RESULT 7
US-09-296-284-7
; Sequence 7, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
; APPLICANT: Choi, Eun-Sung

APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase. Genes
TITLE OF INVENTION: and Methods of use thereof
FILE REFERENCE: 1533.08/0000
CURRENT APPLICATION NUMBER: US/09/296.284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 4830
TYPE: DNA
ORGANISM: Gluconobacter suboxydans
US-09-296-284-7

Query Match 3.0%; Score 18; DB 3; Length 4830;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

274 GCGCCCCCACCCTCAATC 291
97 GCGCCCCCACCCTCAATC 114

RESULT 8
US-09-337-307A-10/c
Sequence 10, Application US/09337307A
Patent No. 6432692
GENERAL INFORMATION:
APPLICANT: Bradford, Christopher A.
APPLICANT: Carver, Lucy A.
APPLICANT: Dunham, Elizabeth E.
TITLE OF INVENTION: Sensitive Biosay For Detecting Agonists Of The Aryl Hydrocarbon
FILE REFERENCE: WARP0105
CURRENT APPLICATION NUMBER: US/09/337.307A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-337-307A-10

Query Match 2.8%; Score 17; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

197 CCACTGCTGACGTGCA 213
30 CCACTGCTGACGTGCA 14

RESULT 9
US-08-199-779-2/c
Sequence 2, Application US/08199779
Patent No. 5681747
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: Kinase C
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5681747ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199.779
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-199-779-2

Query Match 2.8%; Score 17; DB 1; Length 1757;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

277 CCCCCACCCCAATCCC 293
273 CCCCCACCCCAATCCC 257

RESULT 10
US-08-578-615A-105/c
Sequence 105, Application US/08578615A
Patent No. 6015892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578.615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-105

Query Match

2.8%: Score 17; DB 3; Length 1757;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCCCCCCAATCCC 293
DB 273 CCCCCCCCCCAATCCC 257

RESULT 11

Sequence 105, Application PC/TUS9407770
GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett and
APPLICANT: Russell T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07770-105

Query Match 2.8%: Score 17; DB 5; Length 1757;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCCCCCCAATCCC 293
DB 273 CCCCCCCCCCAATCCC 257

RESULT 12

US-08-199-779-1/C
Sequence 1, Application US/08199779
Patent No. 5681747
GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,779
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-199-779-1

Query Match 2.8%: Score 17; DB 1; Length 1812;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCCCCCCAATCCC 293
DB 328 CCCCCCCCCCAATCCC 312

RESULT 13

US-08-578-615A-104/C
Sequence 104, Application US/08578615A
Patent No. 6015892
GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892r1s LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia

Query Match 2.8%: Score 17; DB 5; Length 1757;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-104

Query Match
Best Local Similarity 100.0%; Score 17; DB 3; Length 1812;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCACCCCAATCCC 293
DB 328 CCCCCACCCCAATCCC 312

RESULT 14
PCT-US94-07770-104/C
Sequence 104, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and
APPLICANT: Russell T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 119 Kinase C
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: MacKiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
```

```
FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07770-104

Query Match
Best Local Similarity 100.0%; Score 17; DB 5; Length 1812;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCACCCCAATCCC 293
DB 328 CCCCCACCCCAATCCC 312

RESULT 15
US-09-146-053-6
Sequence 6, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MGI103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 45546
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-6

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 45546;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 ACCGCTACGCCAGCCC 381
DB 22991 ACCGCTACGCCAGCCC 23007

Search completed: September 25, 2003, 11:55:03
Job time : 55 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:03:44 : Search time 54 Seconds
(without alignments)
4896.083 million cell updates/sec

Title: US-09-809-545A-1_COPY_545_1143

Perfect score: 599
Sequence: 1 aaagcgcgcgaacccctac.....acaacgtttgtccatcat 599

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/lna/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/lna/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/lna/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/lna/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	11.7	2372	3	US-09-145-391-1
2	18	3.0	615	3	US-09-296-284-29
3	18	3.0	664	3	US-09-296-284-28
4	18	3.0	3364	4	US-09-930-181-3
5	18	3.0	3431	4	US-09-632-098-1
6	18	3.0	3468	4	US-09-632-098-3
7	18	3.0	4830	4	US-09-296-284-7
8	17	2.8	36	4	US-09-337-307A-10
9	17	2.8	1757	1	US-08-199-779-2
10	17	2.8	1757	3	US-08-578-615A-105
11	17	2.8	1757	5	PCT-US94-07770-105
12	17	2.8	1812	1	US-08-199-779-1
13	17	2.8	1812	3	US-08-578-615A-104
14	17	2.8	1812	5	PCT-US94-07770-104
15	17	2.8	45546	4	US-09-146-053-6
16	17	2.8	536165	4	US-09-214-808-1
17	16	2.7	390	4	US-09-328-352-2282
18	16	2.7	429	4	US-09-252-991A-1762
19	16	2.7	437	1	US-08-631-200-3
20	16	2.7	437	1	US-08-631-200-4
21	16	2.7	437	1	US-08-631-200-5
22	16	2.7	437	1	US-08-829-553-3
23	16	2.7	437	1	US-08-829-553-4
24	16	2.7	437	1	US-08-829-553-5
25	16	2.7	437	2	US-08-922-267A-3
26	16	2.7	437	2	US-08-922-267A-4
27	16	2.7	437	2	US-08-922-267A-5

28	16	2.7	437	2	US-08-936-707A-3	Sequence 3, Appli
29	16	2.7	437	2	US-08-936-707A-4	Sequence 4, Appli
30	16	2.7	437	2	US-08-936-707A-5	Sequence 5, Appli
31	16	2.7	437	2	US-08-936-706A-3	Sequence 3, Appli
32	16	2.7	437	2	US-08-936-706A-4	Sequence 4, Appli
33	16	2.7	437	2	US-08-936-706A-5	Sequence 5, Appli
34	16	2.7	437	3	US-09-248-203-3	Sequence 3, Appli
35	16	2.7	437	3	US-09-248-203-4	Sequence 4, Appli
36	16	2.7	437	3	US-09-248-203-5	Sequence 5, Appli
37	16	2.7	437	3	US-09-406-071-3	Sequence 3, Appli
38	16	2.7	437	3	US-09-406-071-4	Sequence 4, Appli
39	16	2.7	437	3	US-09-406-071-5	Sequence 5, Appli
40	16	2.7	437	3	US-08-905-223-86	Sequence 86, Appli
41	16	2.7	480	1	US-08-630-592-5	Sequence 5, Appli
42	16	2.7	480	1	US-08-714-991-5	Sequence 5, Appli
43	16	2.7	480	3	US-09-032-365A-5	Sequence 5, Appli
44	16	2.7	833	2	US-08-837-029-1	Sequence 5, Appli
45	16	2.7	918	4	US-09-107-532A-2095	Sequence 2095, Ap

ALIGNMENTS

```
RESULT 1
US-09-145-391-1
; Sequence 1, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulist, Stefan M.
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-145-391-1

Query Match          11.7%; Score 70; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 6.2e-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 GATCCAGACTAGAGCCATGTCGATGATGTCGTCCTTCATTCAGAGCT 560
DB 2133 GATCCAGACTAGAGCCATGTCGATGATGTCGTCCTTCATTCAGAGCT 2192
QY 561 AGTATATACC 570
DB 2193 AGTATATACC 2202

RESULT 2
US-09-296-284-29
; Sequence 29, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
; APPLICANT: Choi, Eun-Sung
; APPLICANT: Rhee, Sang-Ki
; APPLICANT: Lee, Eun-Hae
; TITLE OF INVENTION: Gluconobacter Suboxydians Sorbitol Dehydrogenase, Genes
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: 1533.0870000
; CURRENT APPLICATION NUMBER: US/09/296, 284A
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 87
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SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-29
```

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Query Match
Best Local Similarity 3.0%; Score 18; DB 3; Length 615;
Pred. No. 8.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 264 GCGCCCCCACCACCAATC 281
Db 48 GCGCCCCCACCACCAATC 65
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```
RESULT 3
US-09-296-284-28
; Sequence 28, Application US/09296284A
Patent No. 6204040
```

```
GENERAL INFORMATION:
APPLICANT: Choi, Eul-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
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```
SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-28
```

```
Query Match
Best Local Similarity 3.0%; Score 18; DB 3; Length 664;
Pred. No. 8.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 264 GCGCCCCCACCACCAATC 281
Db 97 GCGCCCCCACCACCAATC 114
```

```
RESULT 4
US-09-930-181-3/C
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; Sequence 3, Application US/09930181
Patent No. 6455292
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```
GENERAL INFORMATION:
```

```
APPLICANT: Origene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 160 101 VI
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (482)..(2239)
US-09-930-181-3
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Query Match
Best Local Similarity 3.0%; Score 18; DB 4; Length 3364;
Pred. No. 8.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 261 GCGCGCCCCCACCACCA 278
Db 261 GCGCGCCCCCACCACCA 278
```

```
Db 3039 GCGCGCCCCCACCACCA 3022
```

```
RESULT 5
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```
US-09-632-098-1
; Sequence 1, Application US/09632098
Patent No. 6420154
```

```
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Balndur, Nand
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
FILE REFERENCE: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 26
```

```
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3431
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (37)...(2442)
US-09-632-098-1
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```
Query Match
Best Local Similarity 3.0%; Score 18; DB 4; Length 3431;
Pred. No. 8.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 266 GCGCCCAACCCCAATCCC 283
Db 2978 GCGCCCAACCCCAATCCC 2995
```

```
RESULT 6
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```
US-09-632-098-3
; Sequence 3, Application US/09632098
Patent No. 6420154
```

```
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Balndur, Nand
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
FILE REFERENCE: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 26
```

```
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (37)...(2472)
US-09-632-098-3
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Query Match
Best Local Similarity 3.0%; Score 18; DB 4; Length 3468;
Pred. No. 8.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 266 GCGCCCAACCCCAATCCC 283
Db 3015 GCGCCCAACCCCAATCCC 3032
```

```
RESULT 7
```

```
US-09-296-284-7
; Sequence 7, Application US/09296284A
Patent No. 6204040
```

```
GENERAL INFORMATION:
APPLICANT: Choi, Eul-Sung
```


APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydians Sorbitol Dehydrogenase. Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.08/0000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 7
LENGTH: 4830
TYPE: DNA
ORGANISM: Gluconobacter suboxydians
US-09-296-284-7

Query Match 3.08; Score 18; DB 3; Length 4830;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

264 GCGGCCCCCACCACATC 281
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97 GCGGCCCCCACCACATC 114

RESULT 8
US-09-337-307A-10/c
Sequence 10, Application US/09337307A
Patent No. 6432892
GENERAL INFORMATION:
APPLICANT: Bradford, Christopher A.
APPLICANT: Carver, Lucy A.
APPLICANT: Dunham, Elizabeth E.
TITLE OF INVENTION: Sensitive Biosay For Detecting Agonists Of The Aryl Hydrocarbon
FILE REFERENCE: MARF0105
CURRENT APPLICATION NUMBER: US/09/337,307A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 10
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-337-307A-10

Query Match 2.88; Score 17; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

187 CCACTGCTGCGAGTGA 203
|||||
30 CCACTGCTGCGAGTGA 14

RESULT 9
US-08-199-779-2/c
Sequence 2, Application US/08199779
Patent No. 5681747
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: Kinase C
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5681747ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,779
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-199-779-2

Query Match 2.88; Score 17; DB 1; Length 1757;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

267 CCCCCACCCCAATCCC 283
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273 CCCCCACCCCAATCCC 257

RESULT 10
US-08-578-615A-105/c
Sequence 105, Application US/08578615A
Patent No. 6013892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Leggaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-105

Query Match 2.8%; Score 17; DB 3; Length 1757;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 CCCCCCCCCCAATCCC 283
DB 273 CCCCCCCCCCAATCCC 257

SUPL 11
T-US94-07770-105/C
Sequence 105, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and
Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

Kinase C

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07770-105

Query Match 2.8%; Score 17; DB 5; Length 1757;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 CCCCCCCCCCAATCCC 283
DB 273 CCCCCCCCCCAATCCC 257

RESULT 12
US-08-199-779-1/C
Sequence 1, Application US/08199779
Patent No. 5681747
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5681747ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

Kinase C

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,779
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-199-779-1

Query Match 2.8%; Score 17; DB 1; Length 1812;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 CCCCCCCCCCAATCCC 283
DB 328 CCCCCCCCCCAATCCC 312

RESULT 13
US-08-578-615A-104/C
Sequence 104, Application US/08578615A
Patent No. 6015892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein KinaseC
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia

STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-104

Query Match 2.8%; Score 17; DB 3; Length 1812;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCCCCACCCCAATCCC 283
DB 328 CCCCCACCCCAATCCC 312

RESULT 14
PCT-US94-07770-104/C
Sequence 104, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and
APPLICANT: Russell T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07770-104

Query Match 2.8%; Score 17; DB 5; Length 1812;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCCCCACCCCAATCCC 283
DB 328 CCCCCACCCCAATCCC 312

RESULT 15
US-09-146-053-6
Sequence 6, Application US/09146053A
Patent No. 639349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Antinopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 45546
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-6

Query Match 2.8%; Score 17; DB 4; Length 45546;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 ACCGCTACGCCACGCC 371
DB 22991 ACCGCTACGCCACGCC 23007

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Job time : 55 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:37:54 ; Search time 166 Seconds
(without alignments)
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Scoring table: OLIGO_NDC
Gapop 60.0 , Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

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Minimum DB seq length: 0

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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	599	100.0	1340	10 US-09-809-545A-1
2	70	11.7	2372	9 US-09-794-591-1
3	48	8.0	60	12 US-09-908-975-7420
4	21	3.5	713	13 US-10-027-632-26954
5	21	3.5	713	13 US-10-027-632-150999
6	20	3.3	414	11 US-09-918-995-9070
7	20	3.3	4684	14 US-10-205-823-106
8	18	3.0	278	10 US-09-783-590-7497
9	18	3.0	332	10 US-09-869-708-535
10	18	3.0	458	11 US-09-918-995-565
11	18	3.0	472	11 US-09-918-995-381
12	18	3.0	472	11 US-09-918-995-25844
13	18	3.0	559	13 US-10-027-632-193231
14	18	3.0	559	13 US-10-027-632-193232
15	18	3.0	586	13 US-10-027-632-131089
16	18	3.0	620	13 US-10-027-632-14363

17	18	3.0	650	13 US-10-027-632-22344	Sequence 22244,
18	18	3.0	2173	14 US-10-102-558-1	Sequence 1, App11
19	18	3.0	2407	13 US-10-027-632-101774	Sequence 101774,
20	18	3.0	2830	12 US-10-267-459-1	Sequence 1,
21	18	3.0	2830	12 US-10-209-059-5	Sequence 1, App11
22	18	3.0	3364	14 US-10-195-072-3	Sequence 3, App11
23	18	3.0	3364	14 US-10-195-071-3	Sequence 3, App11
24	18	3.0	3431	12 US-10-177-308-1	Sequence 1, App11
25	18	3.0	3468	12 US-10-177-308-3	Sequence 3, App11
26	18	3.0	3582	12 US-10-199-672-465	Sequence 465,
27	18	3.0	3582	12 US-10-187-749-465	Sequence 465,
28	18	3.0	3582	12 US-10-194-457-465	Sequence 465,
29	18	3.0	3582	12 US-10-184-642-465	Sequence 465,
30	18	3.0	3582	12 US-10-196-747-465	Sequence 465,
31	18	3.0	3582	12 US-10-173-689-465	Sequence 465,
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35	18	3.0	3582	12 US-10-173-694-465	Sequence 465,
36	18	3.0	3582	12 US-10-173-698-465	Sequence 465,
37	18	3.0	3582	12 US-10-173-699-465	Sequence 465,
38	18	3.0	3582	12 US-10-173-707-465	Sequence 465,
39	18	3.0	3582	12 US-10-174-569-465	Sequence 465,
40	18	3.0	3582	12 US-10-174-583-465	Sequence 465,
41	18	3.0	3582	12 US-10-174-587-465	Sequence 465,
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43	18	3.0	3582	12 US-10-174-591-465	Sequence 465,
44	18	3.0	3582	12 US-10-175-336-465	Sequence 465,
45	18	3.0	3582	12 US-10-175-742-465	Sequence 465,

ALIGNMENTS

RESULT 1
US-09-809-545A-1
: Sequence 1, Application US/09809545A
: Patent No. US20020110804A1
: GENERAL INFORMATION:
: APPLICANT: Stanton, Lawrence W.
: APPLICANT: White, R. Tyler
: TITLE OF INVENTION: SECRETED FACTORS
: FILE REFERENCE: SCIOS.017A
: CURRENT APPLICATION NUMBER: US/09/809, 545A
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 84
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1340
: TYPE: DNA
: ORGANISM: Rattus norvegicus
US-09-809-545A-1

Query Match 100.0%; Score 599; DB 10; Length 1340;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	545	AAAAGCGCGTGAACCCCTACACCAATGCTGGAATTAATCCAGTTGTGGCCGCTCT	604
QY	61	ACAGCCCGCACTTATGACGACGAGTGTGTCGACAGCCCAACAGAGGATCTT	120
DB	605	ACAGCCCGCACTTATGACGACGAGTGTGTCGACAGCCCAACAGAGGATCTT	664
QY	121	CCATGTACAGTGGCCCGAGTTCACTTGTATATACCTTGCATAGCCCTGCTTCATATC	180
DB	665	CCATGTACAGTGGCCCGAGTTCACTTGTATATACCTTGCATAGCCCTGCTTCATATC	724
QY	181	CGGCGCCGCACTGCTGACGACGATACAGGAGGCTCACTTGCAGGCGCGTGCACCG	240
DB	725	CGGCGCCGCACTGCTGACGACGATACAGGAGGCTCACTTGCAGGCGCGTGCACCG	784

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Db	845	TGTATCAAGAGCCACT <td>GTATGAGCAATTAATTGCTACAGGGTGTTTACGCTGCATACCGCT</td> <td>904</td> <td></td>	GTATGAGCAATTAATTGCTACAGGGTGTTTACGCTGCATACCGCT	904	
QY	361	ACGCCCAAGCCACCCCTG <td>CACTGCTGCTGCTTACAGTGAACGATTACGAGACAGATTATAG</td> <td>420</td> <td></td>	CACTGCTGCTGCTTACAGTGAACGATTACGAGACAGATTATAG	420	
Db	905	ACGCCCAAGCCACCCCTG <td>CACTGCTGCTGCTTACAGTGAACGATTACGAGACAGATTATAG</td> <td>964</td> <td></td>	CACTGCTGCTGCTTACAGTGAACGATTACGAGACAGATTATAG	964	
QY	421	CTGGCGAACCCTTACC <td>CACACACACTTGGTCCAGCCCCCAACCTACGGCGTTGGTGGCCATGA</td> <td>480</td> <td></td>	CACACACACTTGGTCCAGCCCCCAACCTACGGCGTTGGTGGCCATGA	480	
Db	965	CTGGCGAACCCTTACC <td>CACACACACTTGGTCCAGCCCCCAACCTACGGCGTTGGTGGCCATGA</td> <td>1024</td> <td></td>	CACACACACTTGGTCCAGCCCCCAACCTACGGCGTTGGTGGCCATGA	1024	
QY	481	ATGCTTTTGGCCCTTGA <td>CCAGATGGCAAGACTATAGAGACATGCTGATATATGAGGCTTCG</td> <td>540</td> <td></td>	CCAGATGGCAAGACTATAGAGACATGCTGATATATGAGGCTTCG	540	
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QY	541	TTCTTTTCTTCAATTC <td>ACAGGCTAGTATATACAAAGGGGGATTAACACCGCTTTTGGTCCATAT</td> <td>599</td> <td></td>	ACAGGCTAGTATATACAAAGGGGGATTAACACCGCTTTTGGTCCATAT	599	
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RESULT 2
US-09-794-591-1
: Sequence 1, Application US/09794591
: Patent No. US20010018198A1
: GENERAL INFORMATION:
: APPLICANT: Puist, Stefan M.
: APPLICANT: Shibata, Hiroki
: TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
: FILE REFERENCE: CE 3093
: CURRENT APPLICATION NUMBER: US/09/794,591
: CURRENT FILING DATE: 2001-02-26
: PRIOR APPLICATION NUMBER: 09/145,391
: PRIOR FILING DATE: 1998-09-01
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2372
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (987)..(1979)
: -09-794-591-1

Query Match      11.7%; Score 70; DB 9; Length 2372;
Best Local Similarity 100.0%; Prd. No. 8,4e-28;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 501 GATGCCAAGACTAGAGCCCATGCTGATGATGATGGGTCTCTGTCCTTCTTCATTCGAGGCT 560
      |||||||
Db 2133 GATGCCAAGACTAGAGCCCATGCTGATGATGATGGGTCTCTGTCCTTCTTCATTCGAGGCT 2192
      |||||||

OY 561 AGTATATACC 570
      |||||||
Db 2193 AGTATATACC 2202

RESULT 3
US-09-908-975-7420
: Sequence 7420, Application US/09908975
: Publication No. US20030165843A1
: GENERAL INFORMATION:
: APPLICANT: SHOSHAN, AVI
: APPLICANT: MASSEMAN, ALON
: APPLICANT: MINTZ, ELI
: APPLICANT: MINTZ, Liat
: APPLICANT: FAIGLER, Slmchon

```

```

? TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPL
? TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
? FILE REFERENCE: 36688-0005
? CURRENT APPLICATION NUMBER: US/09/908,975
? CURRENT FILING DATE: 2001-07-20
? PRIOR APPLICATION NUMBER: US 60/287,724
? PRIOR FILING DATE: 2001-05-02
? PRIOR APPLICATION NUMBER: US 60/221,607
? PRIOR FILING DATE: 2000-07-28
? NUMBER OF SEQ ID NOS: 32337
? SOFTWARE: Patentin version 3.0
? SEQ ID NO 7420
? LENGTH: 60
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-908-975-7420

Query Match      8.0%; Score 48; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 9,2e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy      501 GATGCCAGACTAGAGCCATGCGATGATGATGGAGTCTGCTTTCTT 548
        |||||||
Db       13 GATGCCAGACTAGAGCCATGCTGATGATGTGGGTCTCTTTCTT 60

```

```

RESULT 4
US-10-027-632-26954/C
: Sequence 26954, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 26954
: LENGTH: 713
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-26954

Query Match          3.5%; Score 21; DB 13; Length 713;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      32 GAATTAAATCCACTGTGGG 52
        |||||||
Db       231 GAATTAAATCCACTGTGGG 211

RESULT 5
US-10-027-632-150999/C
: Sequence 150999, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150999
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-150999
```

```

Query Match          3.5%; Score 21; DB 13; Length 713;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      32 GAATTAATCACTGTGGG 52
        |||||||
Db      231 GAATTAATCACTGTGGG 211
```

```

RESULT 6
US-09-918-995-9070
; Sequence 9070, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9070
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(414)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-9070
```

```

Query Match          3.3%; Score 20; DB 11; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      144 CTGTATATCTTCTGCAAT 163
        |||||||
Db      180 CTGTATATCTTCTGCAAT 199
```

```

RESULT 7
US-10-205-823-106
; Sequence 106, Application US/10205823
; Publication No. US20030108963A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glat, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-106
```

```

Query Match          3.3%; Score 20; DB 14; Length 4684;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      144 CTGTATATCTTCTGCAAT 163
        |||||||
Db      3962 CTGTATATCTTCTGCAAT 3981
```

```

RESULT 8
US-09-783-590-7497
; Sequence 7497, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7497
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
```

RESULT 10
US-09-918-995-565/c
; Sequence 565, Application US/09918995
; Publication No. US20030073623A1

; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756


```
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 25844
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-25844
```

```
Query Match
Best Local Similarity 100.0%; Score 18; DB 11; Length 472;
Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
261 GCGGCGCCGCCACCCCA 278
|||||
Db 242 GCGGCGCCGCCACCCCA 259
```

```
RESULT 13
US-10-027-632-193231/C
; Sequence 193231, Application US/10027632
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 193231
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-193231
```

```
Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 559;
Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 100 AGGCCAACGAGGAGAT 117
|||||
Db 461 AGGCCAACGAGGAGAT 444
```

```
RESULT 14
US-10-027-632-193232/C
; Sequence 193232, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
```

```
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 193232
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-193232
```

```
Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 559;
Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 100 AGGCCAACGAGGAGAT 117
|||||
Db 461 AGGCCAACGAGGAGAT 444
```

```
RESULT 15
US-10-027-632-131089/C
; Sequence 131089, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 131089
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-131089
```

```
Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 586;
Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 321 GGCAATTAATTGCTACAG 338
|||||
Db 292 GGCAATTAATTGCTACAG 275
```

Search completed: September 25, 2003, 11:50:50
Job time : 166 secs
